Sequence 45, Appl Sequence 38, Appl Sequence 36, Appl Sequence 172673, Sequence 1751, Ap Sequence 2089, Ap Sequence 1, Appli Sequence 1, Appli

Sequence 1510, Apples Sequence 1525, Apples Sequence 116903, Sequence 116903, Sequence 272961, Sequence 272961, Sequence 270907, Sequence 111036, Sequence 111036, Sequence 111036, Sequence 1, Apples Sequence 1, Appli Sequence 1, Appli

Sequence 1, Appli Sequence 5437, Ap Sequence 5483, Ap

ALIGNMENTS

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Gaps 0

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Sequence 53, Sequence 2, Al Sequence 30, Al

US-09-873-676-30

14 13

Result No. Sequence

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Sequence 34, Application US/10292418

Publication No. US20030139365A1

GENERAL INFORMATION:

APPLICANT: Lo, Kin-Ming

APPLICANT: Li, Yue

APPLICANT: Gillies, Stephen D

TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as

TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as

TITLE OF INVENTION: Immunofusins

FILE REFERENCE: LEX-006C1

CURRENT APPLICATION NUMBER: US/10/292,418

CURRENT FILING DATE: 1999-08-25

PRIOR PLING DATE: 1999-08-25

PRIOR PLING DATE: 1999-08-25

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 34

LENGTH: 552
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14 US-10-131-241-45

18 US-10-131-241-48

19 US-10-292-418-38

19 US-10-292-418-36

13 US-10-292-418-36

14 US-10-156-761-1751

12 US-10-156-761-1751

12 US-10-143-715-1

10 US-09-867-701-1510

10 US-09-867-701-1525

11 US-10-027-632-152034

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13 US-10-027-632-12611

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14 US-10-027-632-1211036

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US-09-824-258-1
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DOCATION: (1).(552)

OTHER INFORMATION: Endostatin

US-10-292-418-34
                                                                                                                                                                                                           TYPE: DNA ORGANISM: Canis familiaris
                              FEATURE:
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Sequence 51, Appl
Sequence 213, Appl
Sequence 2171, Appl
Sequence 4, Appl
Sequence 64, Appl
Sequence 144, Appl
Sequence 59, Appl
Sequence 59, Appl
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5967.841 Million cell updates/sec
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                                                                                                                                                            August 17, 2003, 16:34:38 ; Search time 310.875 Seconds
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| cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-880-107-113
US-09-880-107-113
US-09-918-995-23271
US-10-060-036-4
US-10-060-036-4
US-10-060-036-144
US-10-060-036-144
US-10-131-241-59
US-10-131-241-59
US-10-131-241-51
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                                                                                                                OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                          OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Qy         282 CT           Qy         282 CT           Db         144 CT           Qy         342 GG           Qy         402 GG           Qy         462 CC           Qy         462 CC           Qy         462 CC           Qy         522 CC           Qy         522 CC           Qy         524 CT           Db         384 CC           Qy         582 GG           Qy         582 GG           Qy         582 CC           Qy         504 CT           Db         384 CC           Qy         582 GG           Qy         582 GG           Qy         582 GG           Qy         582 CC           PRIOR PRILING           PRIOR PRILING           PRIOR PRILING           PRIOR PRILING	### ### ##############################	09 312 GGTGCCCTCGTCACCTCACACCACACACACACACACACAC
% a	222 AGCGGACTTCCAGTGCTTCCAGCAGGCGCGCGCGGGGCTGGCCGGCACCTTCCGGGC 281	361
G & G	CTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATCGTGCGCCGCCGGCGGCCGCCGCCGCCGCCGCCGCCGCC	421 GGCCCCGGAAGAGCGTGTGGCACGCTCCCACCCCAGCGGGCGCCGCTTGACCGACAGCT 539 ACTGCGACGTGGGGACGGACGGAGGCCCCGCCACCGGGGGGCGCGGCGCTGACCGGCTGGGTGTGGGTGTGGGTGTGGTGGTGGGGGGGG

Length 3394;

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Score 35;
Pred. No.
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                     4.2%; Sccilarity 100.0%; Pr
Conservative 0;
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Matches 29; Conservative
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NAME/KEY: misc_feature
LOCATION: (1)...(297)
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                        Query Match
Best Local Similarity
Matches 35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-918-995-23271
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481 ACTGCGAGACGTGGCGGACGGAGGCCCCGGCGACCGGGCAGGCGTCGTCGCTGCTGG 540
                                                                      Gaps
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US-09-880-107-713
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OCCALEY, JOSEPH G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Generf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-NO
CURRENT FELLING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-66-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR PILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 713
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Sequence 2178, Application US/09880107

Sequence 2178, Application US/09880107

Septemt No. US2020142981A1

SEGNERAL INFORMATION:

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer, PILE REPERDICE: 4921-5038 WO.

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR SPLING DATE: 2000-06-14

SPRIOR FILING DATE: 2000-06-14

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIN Ver. 2.1
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                                                                                                                                        659 TCGAGAACAGCGTCATGACCTCCTTCTCCAAG 690
                                                                                                                                                                601 TCGAGAACAGCGTCATGACCTCCTTCTCCAAG 632
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                                                                                                                                                                                                                                                                                                      Sequence 713, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 3394
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPRENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1999-01-20
PRIOR PILING DATE: 1999-01-20
NUMBER: OF SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23271
LENGTH: 297
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100.0%; Pred. No. 0.00017;
tive 0; Mismatches 0; Indels
                                                                                                               Indels
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Publication No US20030073144A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael D.
APPLICANT: Persing, David H.
APPLICANT: Hersing, David H.
APPLICANT: Holer, William T.
APPLICANT: HOLE
DB 10; L
1.3e-07;
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                                                                                                               Mismatches
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CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23271, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
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US20030114370A1
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US-10-042-347-6
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US-10-131-241-59
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                                                                                                           Sequence 64, Application US/10060036
; Bedication No. US20030073144A1
; GENERAL INFORMATION:
   APPLICANT: Benson, Darin R.
; APPLICANT: Locate, Michael D.
; APPLICANT: Decas, Michael J.
; APPLICANT: Dering, William T.
; APPLICANT: Dering, William T.
; APPLICANT: OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS OF PANCREATIC CANCER; FILE REFERENCE: 210121:566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SEQ ID NO 64
; SEQ ID NO 64
; LENGTH: 574
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APPLICANT: Kalos, Michael D.
APPLICANT: Lados, Michael J.
APPLICANT: Lodos, Michael J.
APPLICANT: Devising, Nation Bayid H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.0012; 
0; Mismatches 0; Indels 0
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100.0%; Pred. No. v
0; Mismatches
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210 CCCTGGCGGCAGATGACATCCTGGCC 236
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US-10-042-347-6
; Sequence 6, Application US/10042347
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Best Local Similarity 100..
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US-10-060-036-64
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                               RESULT 8
US-10-060-036-64
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GENERAL INFORMATION:

APPLICANT: O'Reilly, Michael S.

APPLICANT: O'Reilly, Michael S.

APPLICANT: Folkman, M. Judah

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide Fri

TITLE OF INVENTION: Thereof

FILE REFRENCE: 05213-0880 (43170-249874)

CURRENT FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1998-05-20

PRIOR FILING DATE: 1998-09-16

PRIOR FILING DATE: 1998-09-16

PRIOR FILING DATE: 1996-10-22

PRIOR FILING DATE: 1996-10-22

PRIOR FILING DATE: 1996-00-2

PRIOR FILING DATE: 1996-00-2

PRIOR FILING DATE: 1996-00-2

PRIOR FILING DATE: 1996-00-02

PRIOR FILING DATE: 1996-00-17

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 534

TUND: NUMBER OF SA
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Publication No. US20030012792A1
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation and Regulating Anglogenesis Using Cancer Markers
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CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-0-21
PRIOR PILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
LENGTH: 537
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Sequence 53, Application US/10131241
Publication No. US20030012792A1
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifere
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3.1%; Score 26; DB 12; Length 549; 100.0%; Pred. No. 0.005; 1.1ve 0; Mismatches 0; Indels
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Fublication No. US20020183253A1
GENERAL INFORMATION
APPLICANT: Campochiaro, Peter A.
APPLICANT: Dixon, Katharine H.
APPLICANT: Dixon, Katharine H.
TITLE OF INVENTION: METHOD FOR TREATING OCULAR
TITLE OF INVENTION: METHOD FOR TREATINO
TITLE OF INVENTION: METHOD FOR TREATINO
CURRENT APPLICATION NUMBER: US/10/080,797
CURRENT APPLICATION NUMBER: US/10/080,797
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 551
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0.005;
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CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-06-06
PRIOR PLING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR PILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 53
LENGTH: 549
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100.0%; Pred. No.
ive 0; Mismatch
                                                                                                                                                 88 GACTTCCAGTGCTTCCAGCAGGCGCG 113
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                                                                                                   226 GACTTCCAGTGCTTCCAGCAGGCGCG 251
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     Query Match 3.19
Best Local Similarity 100.(
Matches 26; Conservative
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Matches 26; Conservative
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Best Local Similarity 100.
Matches 26; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Human
US-10-080-797-2
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US-10-080-797-2
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                                                                                                                                     APPLICANT: O'Reilly, Michael S.
APPLICANT: O'Reilly, Michael S.
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide Fr
TITLE OF INVENTION: Thereof
FILE REFERENCE: 05213-0880 (43170-249874)
CURRENT APPLICATION NUMBER: US/10/042/347
CURRENT PILLING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 09/315,689
PRIOR PILLING DATE: 1998-10-30
PRIOR PLILING DATE: 1998-10-30
PRIOR PLILING DATE: 1998-00-16
PRIOR APPLICATION NUMBER: US 09/154,302
PRIOR PLILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: US 60/005,835
PRIOR APPLICATION NUMBER: US 60/005,835
PRIOR PLILING DATE: 1995-10-23
PRIOR PLILING DATE: 1996-10-23
PRIOR PLILING DATE: 1996-00-16
PRIOR PLILING DATE: 1996-00-17
PRIOR PRILING DATE: 1996-00-17
PRIOR PLILING DATE: 1996-00-17
PRIOR PLILING DATE: 1996-00-17
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APPLICANT: Lo, Yue
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION IMMER: US/10/292,418
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
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100.0%; Pred. No. 0.005;
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                                                                     Sequence 4, Application US/10042347
Publication No. US20030114370Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10292418
Publication No. US20030139365A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 100.
Matches 26; Conservative
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US-10-042-347-4
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LOCATION: (1)
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LENGTH: 546
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                       RESULT 12
US-10-042-347-4
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US-10-292-418-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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셤 ò

Search completed: August 17, 2003, 19:58:08 Job time: 320.875 secs

Sequence 16110, A

Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 12260, A Sequence 5583, Ap Sequence 2533, Ap Sequence 2385, Ap Sequence 11220, A Sequence 14122, A

Sequence 797, App Sequence 14035, A Sequence 2299, Ap Sequence 14188, A

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Perfect score:

Run on:

Sequence:

Word size :

Searched:

Database :

Result Š.

0 0 0 0 0 0 0

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0; Indels
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Patent No. 5643783
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF NUMBER OF SEQUENCES:
CORRESPONDENCE 39
CORRESPONDENCE ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
               3 US-09-103-840A-2

3 US-09-103-840A-1

3 US-09-103-840A-1

3 US-09-103-840A-1

US-09-252-991A-16260

US-09-252-991A-5585

US-09-252-991A-5585

US-09-252-991A-5513

US-09-252-991A-5513

US-09-252-991A-2535

US-09-252-991A-12208

US-09-252-991A-12208

US-09-252-991A-12208

US-09-252-991A-1429

US-09-252-991A-1429

US-09-252-991A-1435

US-09-252-991A-1435

US-09-252-991A-1435

US-09-252-991A-1435

US-09-252-991A-1435
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   US-09-252-991A-16110
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Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 35; Conservative 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 02110-2804

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WOTGHEFFECT (Version 5.1)

CURRENT APPLICATION DATA:

FILING DATE: December 1, 1993

CLASSIFICATION NUMBER: US/08/159,784

FILING DATE: December 1, 1993

CLASSIFICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: JOHN F. Freeman

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 00246/170001

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
2028
4403765
4403765
4411529
4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 10, Appl
Sequence 9, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 6, Appli
Sequence 4, Appli
Sequence 30, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appli
Sequence 3, Appli
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                                                                                                                         (without alignments)
4332.442 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, 1
Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4,
                                                                                                         August 17, 2003, 16:25:28 ; Search time 84.4574 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Sequence 1
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -08-956-307B-11
-09-252-991A-16492
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-08-956-307B-10
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US-09-315-689-6

US-09-206-059-30

US-08-70-379-16

US-08-70-379-16

US-09-298-568-1

US-09-298-568-1

US-09-298-568-1

US-09-197-636-1

US-09-197-636-1
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                                                                              OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                    US-09-938-391-1
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1557
1785
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Gaps

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Length 3394;

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US-09-206-059-30
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Patent No. 6346510
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: FOlkman, Judah
APPLICANT: FOlkman, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
CURRENT APPLICATION UNMER: US/09/315,689
CURRENT APPLICATION UNMER: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 6
LENGTH: 534
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o, 1e-06;
o, Indels
Sequence 1, Application US/08159784
Patent No. 5643783
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF NUMBER OF SEQUENCES:
CORRESPONDES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3987 Argraarccrcaagaaaraaaaggaagccaaagag 4021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%; Scor.
100.0%; Pred. No. 10
                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDPEFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REPRENCE/DOCKET NUMBER: 0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-09-315-689-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: De CLASSIFICATION:
                                                                                                                                                                                     Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-315-689-6
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Sequence 30, Application US/09206059

Patent No. 6201104

GENERAL INFORMATION:

APPLICANT: MacDonald, Nicholas

APPLICANT: MacDonald, Nicholas

TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and

TITLE OF INVENTION: Proteins and Methods of Use

TITLE OF INVENTION: Proteins and Methods of Use

CURRENT APPLICATION NUMBER: US/09/206,059

CURRENT APPLICATION NUMBER: US/09/206,059

CURRENT PILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 30

LENGTH: 552
                                                           ö
                                                                                                                                                                                                                                                    Sequence 4, Application US/09315689
Patent No. 6346510
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
                                                         Gaps
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0
           Score 26; DB 4; Length 534;
Pred. No. 0.013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 546; 0.013;
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3.1%; Scor.
100.0%; Pred. No. vo.
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                                                                                                    226 GACTICCAGIGCITCCAGCAGGCGCG 251
                                                                                                                                               76 GACTICCAGIGCTICCAGCAGGGGGG 101
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US-08-770-379-16/c
; Sequence 16, Application US/08770379
; Patent No. 5849564
; GENERAL INFORMATION:
APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.1%; Soc
Best Local Similarity 100.0%; Pi
Matches 26; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.(
Matches 26; Conservative
           Query Match
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-315-689-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE DE INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE DE INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REPERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER PILING DATE: 1998-11-19
NUMBER OF SEO ID NOS: 3
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18;
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PatentIn Release #1.0, Version #1.30
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; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Scot. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.100; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19;
Pred. No.
                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
FILING DATE:
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; Sequence 16, Application US/09230371A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%; bc.
100.0%; Pre
0;
                                                                                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 4518:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
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Bohenzky, Roy A
Russo, James J
Edelman, Isidore S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 801 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.3
Best Local Similarity 100.
Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE:
US-08-757-669A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-298-568-3/c
SOFTWARE:
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APPLICANT:
APPLICANT:
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                                                   APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Rober J.
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 801;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%; Score 19; DB
100.0%; Pred. No. 18;
ive 0; Mismatches
                                                                                                                                                                                                           E: Cooper & Dunham LLP
1185 Avenue of the Americas
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08757669A
Patent No. 6183751
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
RECISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                716 CGGGGGAGGGGGCGCCGC 734
                             Isidore S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 801 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.31
Best Local Similarity 100.0
Matches 19; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
: U.S.A.
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MOLECULE TYPE: D'
                                                                                                                                                                                                                                                                            New York
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APPLICANT:
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16;
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                                                                                                                                     Indels
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0
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
                                                                                   Query Match 2.3%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 16; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 31-041.1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09197636
Patent No. 6239267
                                                                                                                                                                                     126 CCACACCACACCACACC 144
                                                                                                                                                                                                                                    324 ccacaccacacaccacacc
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COUNTRY: US
ZIP: 19482-0980
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"AUTHER: IBM COMPATIBLE
TOWN TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: G
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TELEFAX: 610-407-0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 4803 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 846169
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
               ; MOLECULE TYPE: cDNA
US-09-197-636-7
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
TILLE REFERENCE: 45185-6-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 801
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.3%; Score 19; DB 4; Length 801; Best Local Similarity 100.0%; Pred. No. 18; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTRY: FACOURTY: US

ZIP: 19482-0960

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURREWARE: FastSEQ for Windows Version 2.0
CURREWARE: 23-NOV-1998
CLASSIFICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR.1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 03-SEP-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 03-SEP-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 03-SEP-1998
APPLICATION NUMBER: UK 981578.4
FILING DATE: 13-MAR.1098
APPLICATION NUMBER: UK 981578.4
FILING DATE: 13-MAR.1098
APPLICATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: CP-30075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09197636
; Patent No. 6239267
; GENERAL INFORMATION:
APPLICANT: HYES, PHILIP
PAPLICANT: HYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716 CGGGGGAGGGGCGCCCGC 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 ceececadesecececes 466
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STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
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TELEX: 846169
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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US-09-197-636-7/c
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICANTE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 2718
LENGTH: 273
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54;
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700553162H1
NAME/KEY: unsure
LOCATION: 88, 189, 238, 243, 246, 255, 260
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Petka, Wendy A.
APPLICANT: Tirrell, David A.
APPLICANT: Wevin P. McGrath
ITILE OF INVENTION: REVERSIBLE HYDROGELS
NUMBER OF SEQUENCES: 24
ADDRESSED: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2718, Application US/09313294A Patent No. 6476212
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225 Franklin Street
                  | ENGTH: 112132
| TYPE: DNA
| ORGANISM: Human
| FEATURE:
| NAME/KEY: misc_feature:
| LOCATION: (1)...(112132)
| OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                          32958 CACCCACACCCACACCCAC 32976
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Patent No. 6090911
                                                                                                                                                                                                                                                                                                                129 CACCCACACCCACACCCAC 147
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Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
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COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskete
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STREET: ...
-mv: Boston
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US-09-313-294A-2718
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  SEQ ID NO 3
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Patent No. 6436689
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: UTGLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CLO00968
CURRENT APPLICATION NUMBER: US/09/741,150
CURRENT APPLICATION NOWER: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 15;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,636
FILING DATE: 23-NOV-1998
CLASSIFICATION:
                                                       GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID
APPLICANT: HAYES, PHILIP
APPLICANT: MEADOWS, HELEN
APPLICANT: DAVIS, JOHN
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: RELIER
ADDRESSE: RELIER
ADDRESSE: RELIER
TITLE OF 10. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9805137.8
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: UK 9815791.0
FILING DATE: 21-UL-1998
APPLICATION NUMBER: UK 9819278.4
FILING DATE: 03-SEP-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GP-30075
TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
                  Sequence 3, Application US/09197636
Patent No. 6239267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 CCACACCCACACCACACC 144
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 19; Conservative
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MEDIUM TYPE: Diskette
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STRANDEDNESS: single
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US-09-197-636-3/c
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US-09-741-150-3
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2.2%; Score 18; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,307B
FILING DATE: 22-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 32,983
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 077880/033001
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUIENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TYPE: Nucleic acid
STRANDEDMESS: single
TYPE: NOLLOCY: linear
MOLECULE TYPE: DNA
US-08-956-3078-10
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Search completed: August 17, 2003, 19:49:19 Job time : 94.4574 secs

qq

OM nucleic - nucleic search, using sw model Run on:

August 17, 2003, 13:17:18 ; Search time 4162.37 Seconds (without alignments) 8147.780 Million cell updates/sec

1 ccctggcgggcagatgacat......aataaaaggaagccaaagag 829 Sequence:

US-09-938-391-1 829 Title: Perfect score:

2888711 segs, 20454813386 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched:

Scoring table:

5777422 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

11. gb ba: \*
23. gb htg: \*
48. gb cm: \*
55. gb ov: \*
66. gb pat: \*
77. gb pat: \*
78. g em\_in:\* em\_mu:\* em\_om:\* em\_or:\* em\_hum: em\_ov:\*

em\_sy:\* em\_htgo\_hum:\* em\_htgo\_mus:\* em\_vi:\*
em\_htg\_inw:\*
em\_htg\_inv:\*
em\_htg\_inv:\*
em\_htg\_inv:\*
em\_htg\_ini:\*
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em\_htg\_ini:\*
em\_htg\_ini:\* em\_htg\_vrt:\* em\_ro:\* em\_sts:\* em\_un:\* em\_pat: \* em\_pl:\*

Pred. No. is the number of results predicted by chance to have a

em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

PAT 06-JUN-2002 canis familiaris (dog) Canis familiaris Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Pissipedia; Canidae; Canis. linear DNA Sequence 1 from Patent EP1191036.
AX399629 AX399629.1 GI:21335409 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AX399629 LOCUS

Sheppard, M.G. and Tong, X. Methods and compositions for diagnosing and treating disorders involving angiogenesis REFERENCE AUTHORS TITLE

PAT 06-JUN-2002

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canis familiaris (dog)
Canis familiaris
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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Methods and compositions for diagnosing and treating disorders
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/organism="Canis familiaris"
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/db_xref="taxon:9615"
_203 c 191 g 83 t
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Patent: EP 1191036-A 3 27-MAR-2002;
Pfizer Products Inc. (US)
Sequence 3 from Patent EP1191036.
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                                           GI:21335410
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Pred. No. 7.8e-100;
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 Patent: EP 1191036-A 1 27-MAR-2002; Pfizer Products Inc. (US)
                                                                                                                                                                   0; Mismatches
                              Location/Qualifiers
                                                                                                                                         100.0%;
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Best Local Similarity 100.
Matches 829; Conservative
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Gaps

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198

120 318 180 378 240 438 300 498 360 558 420

258 9

mRNA linear PRI 08-JUL-2002 type XVIII, alpha 1, clone BC033715 2637 bp Homo sapiens, Similar to collagen, IMAGE:4425380, mRNA, partial cds. RESULT 3 BC033715 LOCUS DEFINITION

RESULT 2 AX399631

618

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Similarity
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                       Best Local
Matches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesla,N.E., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Maskrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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GDRGSRGREKADPKKDPKQPGLLPGPPPGPVYVSEQDGSVLSVPGPERGRPGFP
GPAGFKGNLGSKGREKGPGRPGPPGPYTPSPGDGSALGPAQKGRPGFPRGPP
GPAGFKGNLGSKGREKGSPGPKGPFFSPFGPFPGPP
GRPGYKGE1GFPGRPGPRGFKGEPGDASLGFGMRGMPGPPGPPGPP
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PARPPSRPPAHSHRDFQPVLHJVALLSPSLGGGMGGTRGAPPGCPQQARAVGLAGTFRAF
LSSRLQDLYSIVRADDRAAVPIVNLKDELLFBSWEALFSGSEGPLKPGARIFSPDGKD
VLRHPTWPQKSVWHGSDPNGRRLTESYCETWRTBAPSATGQASSLGGRLLGGSAASC
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GDRGDAGQKGERGEPGGGFFCSSLPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPP
GPPGIGYEGRQGPPGPPGPPGFPGPFTPQTISVPGPPGPPGPPGPPGFPGTMGASSGVR
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GHKGSKGAPGPAGARGESGLAGAPGPAGPPGPPGPPGPPGPPGPPGPPGDPGDPGSGGGPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LWATRQAMLGQVHEVPEGWLIFVAEQEELYVRVQNGFRKVQLEARTPLPRGTDNEVAA
                                                                                                             Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                        Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 68 Row: e Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
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/product="Similar to collagen, type XVIII, alpha 1"
/protein_id="AAH33715.1"
/db_xref="GI:21708149"
                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Concact: MGC help desk
Email: cgapbs-r@mail.inh.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9666"
/clone="IMAGE:4425380"
/tissue_type="Kidney, hypernephroma"
/clone_lib="NHH MGC_89"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                       GI:21708148
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                                                                  Homo sapiens (human)
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                     BC033715.1
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ORIGIN
                                                                                     ORGANISM
                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
ACCESSION
                VERSION
KEYWORDS
                                                                                                                                                          REFERENCE
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AF018082 S408 bp mRNA linear PRI 18-MAR-1998 Home sapiens type XVIII collagen (COL18A1) mRNA, alternatively spliced, short form, complete cds.
AF018082.1 GI:2920536
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                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                           2004 CAGCAGGCGCGGGCCCTGGGGGCACCTTCCGCGCCTTCCTGTCCTGCCCTG
                                                                                                          2124 AAGGACGAGCTGCTGTTTCCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG
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                                                                                                                                                                                                           121 CCCGTCCACACCCACACCCACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                        241 CAGCAGGCGCGCGCGCGCGGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTG
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                                                                                                                                                                                                                                                                                                                                       CTGAACAGCCCGCAGCCGGCGCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC
                                           39;
  Length 2637;
                                         Indels
                                       0; Mismatches 152;
  DB 9;
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                     2e-57
Score 504.8;
Pred. No. 2e-
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60.9%;
                                         665; Conservative
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VERSION
KEYWORDS
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720

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AF018081 5929 bp mRNA linear PRI 18-MAR-1998 Homo sapiens type XVIII collagen (COL18A1) mRNA, alternatively spliced, long form, complete cds.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

(bases 1 to 5929)
Saarela,J., Yilkaryppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T.
Complete primary structure of two variant forms of human type XVIII
collagen and tissue-specific differences in the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                              1741 Aaggacgacricricrirricccagcrigagagacrcraricricagacrcradagacrccacra
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Saarela,J., Ylikarppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T.
Direct Submission
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                                                                     3561 CTCAACAGCCCCTGTCAGGGGGATGCGGGGCATCCGCGGGGCCGACTTCCAGTGCTTC
                                                                                                                                                                                 301 CAGGACCTCTACAGCATCGTGCGCCGCGCCGACCGCACCGGGGTGCCCGTCGTCGACCTC
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EGGFGVLFATTDSAQAWLLGVKLSGVQDGHQDISLLYTEPGAGQTHTAASFRLPAFVG
QWTHLALSVAGGFVALYVDCEBFGNRPLARSSRGLELEFGAGLFVAQAGGADPDKFQG
VIAELKVRRDPQVSPWHCLDEEGDDSDGAFGDSGSGLGDARELLREETGAALKPRLPA
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RHPTWPQKSVWHGSDPNGRRLTESYCETWRTBAPSATGQASSLLGGRLLGQSAASCHH
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                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 540a, Sarala, J., Ylikarppa, R., Rehn, M., Purmonen, S. and Pihlajaniemi, T. Complete primary structure of two variant forms of human type XVIII collagen and tissue-specific differences in the expression of the
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DSNVFAESSRPGPPGLPGNQGPPGPKGAKGEVGPPGPPGPPFPPFLQLEAEMKGEKGD
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Saarela,J., Ylikarppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T.
Direct Submission
Submitsed (28-401-1997) Dept. of Medical Biochemistry, University
of Oulu, Kajaanintie 52 A, Oulu 90220, Finland
Location/Qualifiers
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/product="trppe XVIII collagen"
/protein_id="AAG19659.1"
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IPEPQGPLPVQPTADTTTHVTPRNGSTERPATAGSPEPPSELEBGQOPTPSAASPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQENGTTLWPSRGIPSSPGAHTTBAGTLPAPTPSPPSLGRPWAPLTGPSVPPPSSERI
SEEVGLLQLLGDPPPQQVTQTDDPDVGLAYVFGPDANSGQVARYHFPSLFFRDFSLLF
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DGKDVLRHPTWPQKSVWHGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGQS
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1 (28-JUL-1997) Dept. of Medical Biochemistry, University Kajaanintie 52 A, Oulu 90220, Finland Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGGCGGGCAGATGACTCGGCCAGCCCCCTCGCCTGGCCGGAGCCCCAGCCCTAC
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                                                                                                                                                                                                                                                                                       "note="alternatively spliced; long form (NC1-493)"
/codon start=1
product="type XVIII collagen"
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Pred. No. 2.6e-57;
0; Mismatches 153; Indels 39;
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                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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of Oulu, Ka
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Lagodal, T. and Yanamoto, J.

Direct Submission

Submitted (d-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazuaa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Hellx Research Institute (HRI) (supported by Japan

KRY Technology Center etc.); 5' - & 3' -end one pass sequencing:

RRI, and Biotechnology Center, National Institute of Technology and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                     1262 AAGGACGAGCTGCTGTTTCCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG
                                                                                                                                         4322 AAGCCCGGGGGACGCATCTTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCACCTGG
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                                                                                                                                                                                                                481 CCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGCGCCCCTGACCGACAGCTAC
                                                                      AAGCCCGGGGCCCGCATCTTCTTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCCTGG
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oligo capping; fis (full insert sequence)
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. L22548"
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Sequence 2178 from Patent WO0229103.
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Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers
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Pred. No. 5.5e-57;
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                                                                                                                                      /mol_type="mRNA"
/db_xref="texaon:9606"
/clone="UTBRU2002964"
/tissue type="uterus"
/clone_lib="UTBRU2"
/note="cloning vector: pMB18SFL3"
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	661 GAGAACAGCTCCTCTCTCCCAAGTACCCCCCCGCGGGCCCACGGACAGGGGGGG 720  2026 GAGAACAGCTTCATGACTCCTTCTCCAAGTAGGCCCGCGGGCCCACGGAGAGG 2085  DD  2026 GAGAACAGCTTCATGACTGCCTCCAAGTAGCCACGCTGGATGCAGATGCAGATGCAGAGG 2085  DD	GAGGGGGCCCGGCAGAAGCATCCGCCGCGCGGG	757GGGCCTGGCGGGACGCTTGCCTGCACCG-TCACGTTTAATGTAATCCTCAAGAAATA 813 QY 2146 CAGGACCTGGCTGCCATACTTCCTGTATATGTAATCCTCAAGAAATA 2205 Db	814 AAAGGAAAGCCAAAAGA 829 QY 	4 from patent US 5643783.  GI:2472748  OY  OY  OY  OY  OY  OY	,	Collagen and uses therefor  Patent: US 5643783-A 4 01-JUL-1997;  Batent: US 5643783-A 4 01-JUL-1997;  Location/Qualifiers  Location/Qualifiers  ACC  668 a 1130 c 1080 g 516 t  Collagents	Sociation   Societ 496.8; DB 6; Length 3394;   Societ 496.8; DB 6; Length 3394;   Cal Similarity 77.1%; Pred. No. 2.1e-56; Indels 39; Gaps 3; REF   CCTGGCGGCAGATGACATCAGCCGGCCCCGGCCTGACGACCCCAACCAA	TGGG 120	CCCGTCCACACCCACACCCACACCCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCC 180 CONTINUE		CAGCAGGCGCGCGGGGGCTGGCCGCACCTTCCGGGCCTCTGTCGTCGCGGCTG 300	CAGGACCTCTACAGCATCGTGCGCCGCCGCCGCGCGCGCG

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GGFFGSSLPGAPGAPGYPGIPGPRGPFGPFGPFGPGPGPGPGPGPGPPGPP

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PVLHLVALNSPLSGGWGIRGADPGCPQQARAVGLAGTPRAFLSRLQDLYSIVRAD

RAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFFAFLSSRLQDLYSIVWHGS

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Pred. No. 9.4e-56;
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/mol type="genomic DNA"
/db_xref="taxon:32630"
/note="mRNA for mIgSP fused
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ARAVGLSGTFRAFLSSRLQDLYSIVBRADRGSYPIVNLKDEVLSPSWDSLFSGSQGQL
OPGARIFSFDGRDVLRHPAPQKSVWHGSDPSGRRLMESYCETWRTETTGATGQASSL
LSGRLLEQXAASCHWSIVLCTENSPMTSFSK"
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ALPRGTGNEVAALQPPLVQLHEGSPYTRREYSYSTARPWRADDILANPPRLPDRQPYP
                                                                                                                                                                                                                          MMU03714 1615 bp mRNA linear ROD 13-AUG-1994
Mus musculus BALB/c alpha 1 type XVIII collagen (COL18A1) mRNA,
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LFHLEAEMKGDKGDRGDAGQKGERGEPGAPGGGFFSSSVPGPPGPPGYPGIPGPKGRS
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Submitted (24-NOV-1993) Marko Rehn, Department of Medical
Biochemistry, University of Oulu, Kajaanintie 52 A Fin-90220, Oulu,
Finland
                                                                                                                                                                                                                                                                                                                                                                                                             frequent interruptions in the collagen chain, alpha 1(XVIII), with frequent interruptions in the collagenous sequence, a distinct tissue distribution, and homology with type XV collagen 2 tissue distribution, and homology with type XV collagen 2 (bases I to 1615)

Loses I to 1615)

Primary structure of the alpha 1 chain of mouse type XVIII collagen, partial structure of the corresponding gene, and comparison of the alpha 1 (XVIII) chain with its homologue, the alpha 1 (XVIII) chain with its homologue, the Jana 1 (XV) collagen chain

J. Biol. Chem. 269 (19), 13929-13935 (1994)
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                                                                Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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/clone_lib="Mouse adult liver cDNA library by M. Rehn"
/dev_stage="adult, 9-10 weeks"
                                                GGCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC
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/product="alpha 1(XVIII)

    1615
    organism="Mus musculus"
/mol_type="mRNA"
    strain="BALB/c"

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/db_xref="GI:487734"
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/standard_name="COL18A1"
/citation=[2]
/citation=[1]</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                              GAGAACAGCTTCATGACTGCCTCC 882
                                                                                                            661 GAGAACAGCGTCATGACCTCCTTC 684
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                   Rehn, M.V. and Pihlajaniemi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
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Mus musculus
Mus musculus
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MMU03714
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1054 CTGCAGGATCTCTATAGCATCGTGCGCCGTGCTGACCGGGGGTCTGTGCCCATCGTCAAC 1113
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                                                                                                                                                                   Gaps
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Length 1615;
                                                                                                                                                           Indels
Score 436.8; DB 10;
Pred. No. 2e-48;
0; Mismatches 192;
        DB 10;
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357

417

1233

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477

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657

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717

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191

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4802 bp mRNA linear ROD 16-APR-2003
Mus musculus procollagen, type XVIII, alpha 1, mRNA (cDNA clone
BCO43697
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Meteria; Rdentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 4802)
Strausberg; N.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Rlausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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                                                                                                                      GGGCCCGTCCACACCCCACACACCCACACACCACACCTCCAGCTGGTGCTGCACCTGGTG
                                                                                                                                                                                                                                          178 GCCCTGAACAGCCCGCAGCCGGGCGGCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGC
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BC043697.1 GI:27882148
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GREDTTDGACRETTGATAGPREKEKGPPGTGTRERGPBGFRDFRSFRQALTFITINKEGS
GREDTIESLIKGPRGPPGPPCPPGLPGEPGRFGTNGSYAPGPAGLPGVPGKTGCPPG
FPGPPGPPGPPGKEGPPGPGRGSVGDVGIPGPRGSKGDLGPIGNFGKSGLAGSPGP
FPGPPPGPPGPPGPAGPDGMGSGSTPLMTTARSBOLGQPGGPGGAGPPGAGSPGP
LPGAKGEVGADGAQTTGPPGPGTAGTAGSPGTKGTRCKGPGEKGNPGKACVGRPGA
GPPGPVITVSSEDKAIVSTPGPEGKPGTAGFPGPKGFKGPKGEKGNPGEKGNPGFKGE
GPPGPVITVSSEDKAIVSTPGPEGKPGYAGFPGPAGPKGEKGNPGEKGNPGFKGEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="QRVPFARASQGLELERGAGLFVGQAGTADPDKFQGMISELKVRK
TPRVSPVHCLDEEDDDEDRASGDFGSGFEESSKSHKEDTSLLPGLPQPPPVTSPPLAG
GSTTEDPRTEETEEDAAVDSIGAETLPGTGSSGAWDEAIQNPGRGLIKGGMKGQKGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGTTFSPDGRALGHPOKGAKGBPGFRGPPGPYGRPGHKGEIGFPGRPGRPGTNGLKGE
KGEPGDASLGFSMRGLPGPPGPPGPPGMPIYDSNAFVESGRPGLPGOOGVQGPSG
PKGDKGEVGPPGPPGQFPIDLFHLEAEMKGDKGDRGDAGQKGERGEPGAPGGGFFSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EELYVRVRNGFRKVLLEARTALPRGTGNEVAALQPPLVQLHEGSPYTRREYSYSTARP
WRADDILANPPRLPDRQPYPGVPHHSSYVHLPPARPTLSLAHTHQDFQPVLHLVALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPLSGGMRGIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSIVRRADRGSVPIVNL
KDEVLSPSWDSLFSGSQGQLQPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLME
SYCETWRTETTGATGQASSLLSGRLLEQKAASCHNSYIVLCIENSFWTSFSK"
04-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPGPPGPPGYPG1PGPKGES1RGPPGPPGPQGPPG1GYEGRQGPPGPPGPPSFPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHRQTVSVPGPPGPPGPPGAMGASAGQVRIWATYQTMLDKIREVPEGWLIFVAER
                                                                                                                                                                                                                                                                                            Abe, N., Muragaki, Y., Yoshioka, H., Inoue, H. and Ninomiya, Y. Identification of a novel collagen chain represented by extensive interruptions in the triple-helical region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                              Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-SEP-1993) Nobuhiro Abe, Okayama University Medical
School, Molecular Biology and Biochemistry; 2-5-1, Shikata-cho,
Okayama, Okayama 700, Japan (Tel:81-86-223-7151(ex.2390),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCCTGGCGGCAGATGACATCCTGGCCGGCCCCCGCGCCTGCTGGACCCCCAGCCCTAC
      ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax:81-86-222-7768)
On Jun 5, 1997 this sequence version replaced gi:467516.
Location/Qualifiers
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   linear
4437 bp mRNA li
collagen, partial cds.
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llarity 73.5%; Pred. No. 1.5e-48;
Conservative 0; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:10090"
/dev_stage="embryo"
/note="clones NA[1,12,286,2611]"
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/product="collagen"
/protein_id="BAA04483.1"
/db_xref="G1.467517"
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1311 c 1345 g 8
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                                                                                                                                                                              Mus musculus
Bukaryota, Metazoa, Chordata,
Mammalia, Butheria, Rodentia,
1 (bases 1 to 4437)
                                                                                                                                                  Mus musculus (house mouse)
                            Mus musculus mRNA for
                                                                                       D17546.1 GI:2160436
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2 (bases 1 to 4437)
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                     DEFINITION
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4158 TICCAGCAAGCCCGAGCCGTGGGGCTGTCGGGCACCTTCCGGGCTTTCCTGTCCTGTAGG 4217
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                                                                                                               118 GGGCCCGTCCACACCCACACACCCACACCCAGGACTTCCAGCTGGTGCTGCACCTGGTG
                                                                                                                                                                                                           178 GCCCTGAACAGCCCGCAGCCGGCGCGCATGCGAGCGGGAGCGGACTTCCAGTGC
                                                                                                                                                                                                                                                            4098 GCACTGAACACCCCCTGTCTGGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGC
                                                                                                                                                                                                                                                                                                              TICCAGCAGCGCGCGCGCGCGGGGCTGGCCGGCACCTTCCGGGGCCTTCCTGTCGTCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                             CTGCAGGACCTCTACAGCATCGTGCGCCGCCGCCGACCGCACCGGGGGGCCCGTCGTCAAC
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                                                             linear
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1 (bases 1 to 4031)

Olsen,B.R. and Oh,S.P.
Collagen and uses therefor
Patent: US 5643783-A 1 01-JUL-1997;
Location/Qualifiers
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Sequence 1 from patent US 5643783.
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Bromstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Schwicheko, Y., Butterfield, Y.S., Krzywinski, M., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chia, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacquelline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (10-2MN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: RAK Plate: 86 Row: k Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="liMAGE:5110177"
/tissue_type="liver, normal: 5 month old male mouse."
/clone_lib="NCI_CGAP_Li9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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llarity 73.5%; Pred. No. 1.4e-48;
Conservative 0; Mismatches 192; 1
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1435 c 1468 g 870 t
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg, R.
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191

819

07-0CT-1997

PAT

4577

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4457

597

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source text: Mus musculus
Location/Qualifiers
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/protein_id="AAA19787.1"
/db_xref="GI:511298"
proteins
Acad. Sci. U.S.A. 91
                                                                                                    organism="Mus musculus"
                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="liver"
                                                                                                                                                                /dev_stage="embryo"
:1. .3867
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les 548; Conservative
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            Proc. Natl. 7
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Original sou
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Oh, S.P., Kamagata, Y., Muragaki, Y., Timmons, S., Ooshima, A. and Olsen, B.R. Isolacion and sequencing of cDNAs for proteins with multiple domains of Gly-Xaa-Yaa repeats identify a distinct family of
                                                                                                                                                                                                 CCCGGGG---CCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGT
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                                                        Length 4031;
                                                       Score 423; DB 6; Length 40
Pred. No. 9.9e-47;
0; Mismatches 150; Indels
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              u
              720
/organism="unknown"
1172 c 1266 g
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                                                          51.0%;
76.9%;
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LOCUS
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VERSION
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SOURCE
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GDVGI PGWTARSBDGLGQPPGSPGLKGPPGVAVGPPGPPGPPGPPGPPGPBGKSGAA
GSPPGWGRKGRKGMPGRSCPSCPLKGPPGPPGPPGIV I YVSSEDKA I VSTPGPBGKP
GYAGFPGPAGPKGBLGSKGEQCLPGFKGEKGEPGPT I FSPDGRRLGHPOKGAKGEPGFR
GYPGPFGRHKGBLGFSRRCBCPTMCLKGRKGEPGPALGFSRRGLGPPRGPEPGPP
GPPGWPI YDSNA FVESGRPQLPGFKGEPGPSSCPKGDRGEVGPPGPPGPPEPGPP
GPPGWPI YDSNA FVESGRPGLPGCQVVQCFSCSVPGPRGPFGPPGPPFILEHLEA
BMKGDRGGDRGCDRGEPGPAPGGGFFSSSVPGPPGPPGPPFILEHLEA
BMKGDRGGDRGCDRGEPGPAPGGGFFSSSVPGPPGPPGPPFILEHLEA
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AQYHFPKLFFRDFSLLFHVRPATEAAGVLFAITDAAQVVVSLGVKLSEVRDGQQNISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYTEPCASQTQTGASFRLPAFVGQWTHFALSVDGGSVALYVDCEEFQRVPFARASQGL
ELERCAGLFVCQAGTADPDKFQGMISELKVRKTPRVSPVHCLDEEDDDEDRASGDFGS
GFEESSKSHKEDTSLLPGLPQPPPVTSPPLAGGSTTEDPRTEETTEEDAAVDSIGAETL
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VPGAQGPPGPPGPDGFDGTPGRDGEPGDPGEDGRPGDTGPQGFPGTPGDVGPKGEKGD
PGI GPRGPPGPPGPPGPSFRQDKLTFI DMEGSGFSGDI ESLKGPRGFPGPPGPPGVPG
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SAGQVRIWATYQTMLDKIREVPEGWLIFVAEREELYVRVRNGFRKVLLEARTALLRGT
GNEVAAFQPPLVQLHEGSPYTRREYSYSTARPWRADDILANPPRLPDRQPYPGVPHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSYVHLPPARPTLSLAHTHQDFQPVLHLVALNTPLSGGMRGIRGADFQCFQQARAVGL
SGTRRALSSRLQDLYSIVRRALNGSVPIVNLKDBVLSPSWDSLFSGSQGQVQPGARI
FSFDGRDVLRHPAMPQKSVWHGSDPSGRRLMESYCETWRTETTGATGQASSLLSGRLL
EQKAAGCHNSYIVLCIENSFWTSFSK"
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                                                                                                                   mRNA
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3652 TGGCCGCAGAAGAGCGTATGGCACGCTCGGACCCCAGTGGGCGGAGGCTGATGGAGAGT 3711
                                                                                                                                                3712 TACTGTGAGACATGGCGAACTGAAACTACTGGGGCTACAGGTCAGGCCTCCTCCTGCTG 3771
3532 CTGAAGGACGAGGTGCTATCTCCCAGCTGGACTCCCTGTTTTCTGGCTCCAGGGTCAA 3591
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Sequence 6, Appli
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Sequence 3, Appli
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Sequence 144, App
Sequence 48, Appl
                                                                                                           August 17, 2003, 16:34:38; Search time 208.125 Seconds (without alignments) 5967.841 Million cell updates/sec
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US-10-042-347-6
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US-0-0873-676-30
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Sequence 2312, Ap Sequence 2650, A Sequence 26500, A Sequence 46928, A Sequence 13617, A Sequence 7869, Ap Sequence 68162, Ap Sequence 68162, Sequence 102776, Sequence 153544,
                                                       Sequence 37, Appl
Sequence 12, Appl
Sequence 4, Appli
Sequence 2133, Ap
Sequence 2313, Ap
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Sequence 220, App
Sequence 1504, Ap
         Sequence 1841, Ap
Sequence 1, Appl
                                 Sequence 17, Appl
                                        Sequence 3, Appli
Sequence 3, Appli
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                          Sequence 11952
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US-10-027-632-294984
US-10-027-632-102776
US-10-106-698-1578
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US-10-156-761-1504
4 US-10-292-418-36
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US-10-198-846-11952
2 US-10-292-418-17
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9 US-09-998-811-12
9 US-09-998-811-12
9 US-09-998-911-12
9 US-09-764-869-2312
1 US-09-918-995-26500
3 US-10-027-652-6500
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US-09-864-766-136-74
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1002
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## ALIGNMENTS

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APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Li, Yue
TILLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TILLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TILLE OF INVENTION: Immunofusins
FILE REFERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 1990-08-25
PRIOR PLILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 AGCGGACTTCCAGTGCTTCCAGCAGCGCGCGCGCGGGGCTGGCCGGCACCTTCCGGGC 143
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100.0%; Pred. No. 7.1e-249;
.ive. 0; Mismatches 0; Indels
Sequence 34, Application US/10292418.
Publication No. US20030139365A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (1)..(552)
OTHER INFORMATION: Endostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.3%;
Best Local Similarity 100.0%
Matches 529; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Canis familiaris
                                                                                     APPLICANT: Lo, Kin-Ming
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Sequence

US-10-131-241-48 US-10-292-418-38

0y         204 GGTGCCGTCGTCAACCTCAAGGACGAGGTCCTCTTCCCCAGCTGGAGGCCTTATTCTC         263           0y         204 GGTGCCCGTCGAACCTCAAGGACGAGGTCTTCTCCCCAGCTGGAGGCCTTATTCTC         263           0y         264 GGGCTCCGAGGGCCAGCTGAAGCCCGGAGCCTTATTCTC         263           0y         264 GGGCTCCGAGGGCCAGCTGAAGCCCGGATCTTTCTTTTGACGGCAGAATGT         323           0y         324 CCTGCAGGCCAGCTGAAGCCCGGAAGAGCTGTGGCACCCGAGGGGCG         383           0y         324 CCTGCAGCACCCGGCTGGCCCGGAAGAGCGTGGCACGCCCCCAGCGGGCG         383           0y         324 CCTGCAGCACCCGGCTGGCCCGGAAGAGCGTGGGCACCCCGGGGCCCCCCAGGGGCG         383           0y         324 CCTGCAGCCCCGCTACTACTCCGGAACGTGGCGACGGCCCCCCGGGCCCCCCCGGCGCCACCCGGGCCACCCGGCCCCCC	US-10-131-241-51  i Sequence 51, Application US/10131241  j Sequence 51, Application US/10131241  j Sequence 51, Application No. US20030012792A1  GENERAL INFORMATION:  APPLICANT: Holaday, John W.  TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial  TITLE OF INVENTION: and Regulating Anglogenesis Using Cancer Markers  FILE REPERENCE: 05213-0344 413170-271565  CURRENT APPLICATION NUMBER: US/10/131,241  CURRENT PILING DATE: 1999-10-06  PRIOR PELING DATE: 1999-10-06  PRIOR PELING DATE: 1999-05-21  PRIOR PELING DATE: 1999-05-22  PRIOR PELING DATE: 1999-05-22  PRIOR SEQ ID NOS: 65  SOFTWARE: Patentin version 3.1  LENCTH: 632  TYPE: DNA  US-10-131-241-51  QUELY MATCH  QUELY MATCH  ROGEL DATE: 1000 B. DATE B. DA	Deal 31, Conservative 1987   100   101   1
144   CTTCCTGTCGCGCGCGCGCGCGCGGGGCCGCGCCGCCCCGCCCC	Qy 504 CTTCGTGGTCCTCCATCAGAACAGCTCATCTCCAAG 552	TYPE: DNA   ORGANISM: Canine sp.   OSTANISM: Caninilarity   100.0%;   Pred. No. 7.1e-249;   DB 14;   Length 552;   Best Local Similarity   100.0%;   Pred. No. 7.1e-249;   Organizative   O.   Organizative   Organizative   Organizative   O.   Organizative   O.   Organizative   O.   Organizative   Organizative   O.   Organizative   Organizative   O.   Organizative   O.   Organizative   O.   Organizative   O.   Organizative   O.   Organizative   O.   Organizative   Organiza

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GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael S.
APPLICANT: O'Reilly, Michael S.
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide Fre
TITLE OF INVENTION: Thereof
FILE OF INVENTION: Thereof
FILE OF INVENTION: Thereof
FILE OF INVENTION: Thereof
FILE REPERROR: 05213-0880 (43170-249874)
CURRENT APPLICATION NUMBER: US 09/315,689
PRIOR APPLICATION NUMBER: US 09/315,689
PRIOR PILING DATE: 1999-05-20
PRIOR PELING DATE: 1998-10-30
PRIOR PLING DATE: 1998-10-30
PRIOR PLING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: US 60/005,835
PRIOR APPLICATION NUMBER: US 60/023,070
PRIOR FILING DATE: 1995-10-23
PRIOR PILING DATE: 1996-00-17
PRIOR PILING DATE: 1996-00-17
PRIOR FILING DATE: 1996-00-17
PRIOR FILING DATE: 1996-00-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
FRANCH: 546
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APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
FILE REPERENCE: LEX-006C1
                                                                                                                                                                                                                                  Length 537;
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                                                                                                                                                                                                                                      4.7%; Score 26; DB 14;
.00.0%; Pred. No. 0.0052;
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                                                                                                                                                                                                                                                                                                        Mismatches
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CURRENT FILING DATE: 2002-11-17
PRIOP NOTICE
                                                                                                                                                                                                                                                                                                                                                                           88 GACTICCAGIGCIICCAGCAGGCGCG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                      76 GACTICCAGIGCTICCAGCAGGCGCG 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10042347
Publication No. US20030114370A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 537
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                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 26; Conservative
                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-241-59
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ORGANISM: Homo sapiens
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US-10-292-418-3
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Publication No. US20030012792A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-05-22
PRIOR FILING DATE: 1999-05-22
PRIOR FILING DATE: 1999-05-22
                                                                                                        541 CGGCAGGCTGCTGGAGCAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCA 600
   481 ACTGCGAGACGTGGCGGACGGAGGCCCCGGCGCCACGGGCAGGCGTCGCTGCTGCTGG 540
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100.0%; Pred. No. 0.0052;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                  601 rccagaacagcercargacerecreeredag 632
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 26, Conserval
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APPLICANT: Sim, Kim L.

TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use FILE REFERENCE: 05213-0378 (43170-259333)

CURRENT APPLICATION NUMBER: US 60/209,065

PRIOR PILING DATE: 2001-06-04

PRIOR FILING DATE: 2000-06-02

PRIOR FILING DATE: 2000-06-05

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 123

SOFTWARE: Patentin version 3.1

SEQ ID NO 30

LEAGTH: 552

LEAGTH: 552
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| Sequence 64, Application US/10060036
| Publication No. US20030073144A1
| GENERAL INPORMATION:
| APPLICANT: Ralos, Michael D. APPLICANT: Lodges, Michael D. APPLICANT: Dearing David H. APPLICANT: Hepler, William T. APPLICANT: Jang, Yugiu
| APPLICANT: Jang, Yugiu
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER TITLE OF INVENTION: WHEBER: US/10/060,036
| CURRENT FILIK DATE: 2002-01-30
| NUMBER OF SEQ ID NOS: 4550
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 64
| CURRENT S74
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                                                                                                                                                                         Length 551;
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100.0%; Pred. No. 0.0051;
trive 0; Mismatches 0
                                                                                                                                                                    4.7%; Score 26; DB 13;
100.0%; Pred. No. 0.0051;
tive 0; Mismatches 0
    SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 26; Conservative
                                                                                                                                                                                                                   26; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-060-036-64
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Best Local Similarity
                      SEQ ID NO 2

LENGTH: 551

TYPE: DNA M

CRGANISM: Human

US-10-080-797-2
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US-09-873-676-30
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US-10-060-036-64
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Sequence 54, Application US/20311241

Sequence 55, Application US/20311241

Sequence 57, Application US/20311292A1

SEQUENCE TO COMPANATION:

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

CURRENT APPLICATION NUMBER: US 09/413,049

PRIOR PILING DATE: 1999-10-06

PRIOR PILING DATE: 1999-05-21

PRIOR PILING DATE: 1999-05-21

PRIOR PILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Version 3.1

SEQ ID NO 53
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Pred. No. 0.0052;
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100.0%; Pred. No. 0.0052;
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Publication No. US20020183253A1
GENERAL INFORMATION:
APPLICANT: Campochiaro, Peter A.
APPLICANT: Dixon, Katharine H.
APPLICANT: Brazzell, Romulus K.
TITLE OF INVENTION: METHOD FOR TREATING OCULAR
TITLE OF INVENTION: NEOVASCULARIZATION
FILE REFERENCE: 4-31881A
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 21
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PRIOR FILING DATE: 1999-08-25
PRIOR PEDLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 3
LENGTH: 549
                                                                                                                                                                                                                                                                  LOCATION: (1)..(549)
OTHER INFORMATION: endostatin
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Best Local Similarity
Matches 26; Conserv
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US-10-131-241-53
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US-10-080-797-2
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                                                                                                                                                                    TYPE: DNA
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APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
APPLICANT: Fortier, Anne H.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer?
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE OF INVENTION WINBER: US/10/131,241
CURRENT APPLICATION NUMBER: US/10/131,241
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-22
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APPLICANT: Ralos, Michael D.

APPLICANT: Lados, Michael D.

APPLICANT: Lados, Michael J.

APPLICANT: Dersing, Michael J.

APPLICANT: Dersing, Vadiu H.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 4551
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100.0%; Pred. No. 0.15;
tive 0; Mismatches 0; Indels
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Pred. No. 0.0035;
0; Mismatches 0
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                                                                               1591 GACTTCCAGTGCTTCCAGCAGGCGCG 1616
                            88 GACTICCAGIGCTICCAGCAGGCGCG 113
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Publication No. US20030073144A1
GENERAL INFORMATION:
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; Sequence 48, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
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ilarity 100.0%; P.
Conservative 0;
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SOFWARE: Patentin version 3.1
SEQ ID NO 48
LENGTH: 540
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Matches 23; Conservative
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CORGANISM: Homo sapiens
US-10-060-036-144
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Best Local Similarity
Matches 26; Conserva
                                                                                                                                                                                         US-10-060-036-144
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                                                                                                                                                                                                                                                                Sequence 45, Application US/10131241

Publication No. US20030012792A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT PAPPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-05-22
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR PILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOCTION OF PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
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; Sequence 2178, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Horne, Darci T.
; APPLICANT: Scherf, Uwe
; APPLICANT: Scherf, Uwe
; APPLICANT: GENERAL ONE
; TILLE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT PILING DATE: 2001-06-14
; PRIOR PILING DATE: 2000-06-14
; PRIOR PILING DATE: 2000-00-02
; NUMBER OF SEQ ID NOS: 3550
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2178
; LENGTH: DATE: 2000-10-02
; LENGTH: APPLICATION NUMBER: US 60/237,054
; PRIOR PILING DATE: 2000-10-02
; LENGTH: APPLICATION NUMBER: US 60/237,054
; PRIOR PILING DATE: 2000-10-02
; LENGTH: DATE: 2000-10-02
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Live 0; Mismatches 0; Indels
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Pred. No. 0.0047;
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100.0%; Pred. No. 0.0051;
tive 0; Mismatches 0
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ORGANISM: Homo sapiens
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US-10-131-241-45
  Best Local Similarity
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US-10-131-241-45
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LENGTH: 900
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Search completed: August 17, 2003, 19:58:14 Job time : 214.125 secs

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Minimum DB Maximum DB

Database

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BF07559 UT-M-FR0-
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AW136127 UT-H-B11-
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BF43605 7p64d10.x
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BY674034 BY674034
BH731921 BH731921
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BH731946 BH731964
BH731948 BH731918
BY660494 BY660494
A7241051 qj95g10.x
BH731968 BH731968
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Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos
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Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics W. M. Keck Center for Comparative Champaign University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone BP230015B10C11 5', mRNA sequence
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                           AI540493
BU610789
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Bos taurus (cow)
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AW464343
 AW464343 BP230015B
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CB444165 695295 MA
                                                                   Search time 2416.32 Seconds (without alignments) 8338.472 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                   August 17, 2003, 16:23:08;
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Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi grows match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.
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1 (bases 1 to 387)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Gasas, B., Wany, D.E., White, J., Cho, J., Pahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohers, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                             /BCKS-Leminal.
/lab host="United"
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/clone_lib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pT773Pac; Site_l: EccRI;
Site_2: NotI; The CDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
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libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
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266182 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
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100.0%; Pred. No. 7.9e-12;
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                                                                                                                                                                 BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 279 Std Error: 0.00
Plate: BP230015B10 row: C column: 11
                                                                                                                                                                                                                                 Seg primer: AGCGGATAACAATTTCACAGGA
High quality sequence stop: 279.
Location/Qualifiers
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/mol_type="mRNA"
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FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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PUBMED
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BF601253
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRIMERS
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                                                                                                                                   /mol type="mmkna"
/db_xref="taxon:9913"
/db_xref="taxon:9913"
/db_xref="taxon:9913"
/lab_bost="mold"
/lab_bost="MARC 3BOV"
/clone lib="WARC 3BOV"
/note="Vector: pcMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from marrow, alveolar
Library made ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
140 c 131 g 64 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 25-APR-2001
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tiscue type="pooled"
/lab host="pooled"
/lab host="DH10B"
/clone lib="WARC 2BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/inche="vector: pCMV SPORT6 tissue from testis, thymus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 387;
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4360
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; L
8.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r Match 5.7%; Score 47; DB Local Similarity 100.0%; Pred. No. 8.1 les 47; Conservative 0; Mismatches
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                                                                                                                 /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Bos taurus"
Plate: 40 row: H column: 7
Seq primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
                                                       Location/Qualifiers
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7

Query Match Best Local

Matches

BASE COUNT ORIGIN

RESULT 4 CB444165/c

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DEFINITION

ACCESSION VERSION KEYWORDS

ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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Tumor Gene Index
Unpublished
Other EST9: maa33112.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage==10 weeks"
/lab_host="0H10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Li10"
/note==0rgan: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Library constructed by Life
Technologies."
                                     Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Josses 1 to 110)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 120)
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National Cancer Institute / National Institute of Dent:
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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5.2e-06;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:3812998"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco
High quality sequence stop: 9
Location/Qualifiers
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                       Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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Best Local Similarity lov..
Best Local 35; Conservative
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ORIGIN
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VERSION
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AUTHORS
TITLE
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AUTHORS
TITLE
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BG151469
KEYWORDS
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BF322807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: FQ78051 row: 1 column: 11
Seq primer: TAGAAGGCACAGTCGAGG.
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Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled From multiple tissues
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semitendonosus muscle, longissimus muscle, pancreas,
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                                                                                                           Length 551;
                                                                                                                                                                                                                                                                                                                                                       CB444165 6BOV Bos taurus cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 others
                                                                                                                                                     0; Indels
                                                                                                                                                                                                    232 CAGTGCTTCCAGCAGGCGCGCGCGCGGGGCTGGCCGGCACCTTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                         DB 10; I
. 8.4e-12;
                                                                                             5.7%; Scc. No. o. 100.0%; Pred. No. o. ... 0; Mismatches
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                     adrenal, and endometrium
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Fax: 402 762 4390
Email: smith@email.marc.usda.gov
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/lab_host="DH10B"
/clone_lib="MARC_6BOV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 657)
                                                                                                                                                   47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Conservative
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                                                                                                                              Similarity
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Gaps

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Dental Research,

RESULT 5 BF322807/c

DEFINITION

ACCESSION VERSION

BASE COUNT ORIGIN

Matches

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Location/Qualifiers
          'lab host="DH10B"
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AI540493
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Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                    made from head/neck tissue; Vector: pAMP1; mRNA made from head/neck tissue, cDNA made by oligo-dT priming. Directionally cloned into UDG sites.
Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA Library Preparation: David B. Krizman, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 138) Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 08-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM197778 Linear EST 08-JUN-20
C0324C07-3 NIA Mouse Undifferentiated ES Cell cDNA Library (Long)
Mus musculus cDNA clone NIA:C0324C07 IMAGE:30007134 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Putative full length read
The vector to vector length is 121
Seq primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaedgsun.grc.nia.nih.gov
Plate: C0334 row. C column: 07
Seq primer: -21M13 Forward
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Other ESTs: C0324C07-5N
Contact: Dawood B. Dudekula
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/db_xref="niaEST:C0324C07-3"
/db_xref="taxon:10090"
/clone="N1A:C0324C07 IMAGE:30007134"
/tissue_type="Undifferentiated ES Cell"
/cell_line="R1 ES cells"
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                                                                                                                                                                                                           /clone="IMAGE:4262301"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_HN20"
/note="Organ: normal_head/
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                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Conservative
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Best Local Similarity
Matches 35; Conserv
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14.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The CDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao (NIA)."
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Junter (Jougy)
Junte
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrpt/mage/image.html
Insert Length: 716 Std Error: 0.00
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone lib="NIA Mouse Undifferentiated ES Cell cDNA Library (Long)"
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High quality sequence stop: 113
POLYA=No.
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/db xref="taxon:10090"
/clone="vI_M="ref0-car-h-11-0-UI"
/tissue_type="whole brain"
/dev stage="embryo 12.5 dpc"
/lab_host="DH10B (Tl phage resistant)"
/clone_llb="will BMAP FCO"
/clone_llb="will BMAP FCO"
/note="Organ: brain; Vector: pYX-Asc; Site_1: BcoR I;
Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose gel: First strand coNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cond primer containing a Not I site. Double stranded cond was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, Dento-Soares@ulowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BUG10789 155 bp mRNA linear EST 20-FEB-2003 UI-M-FCO-car-h-11-0-UI.rl NIH BMAP_FCO Mus musculus cDNA clone
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                                                                                                                                                         /clone_lib="NCI_CGAP_Utl"
//note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Clone unidirectionally. Primer: Oligo dT:
Average insert size 1.75 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 155)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                 /tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors" /lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                             Length 142;
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5.3e-06;
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100.0%; Pred. No. ...
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/mol_type="mRNA"
/strain="C57BL/6"
organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                /clone="IMAGE:2209800"
                     /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                       11538-014"
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Вb

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DNA Sequencing by: Wandington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp//lmage/hmage.html
Insert Length: 1209 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stopp: 144.
sequence located between the Not I site and the polyA tail.
'is ITGAGAGGC. This library was created for the
University of Lowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Instututes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A1991894 1108 DEAR 158 bp mRNA linear EST 08-MAR-2000 ws42a08.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2499830 3' similar to contains TAR1.tl MER22 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 158)
NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                   Length 155;
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                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                   Score 35; DB 13; I
Pred. No. 5.3e-06;
                                                                                                                                                                                                                                                                                                                                                               92 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 126
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                                                                                                                                                                                                              4.2%; Scor.
100.0%; Pred. No. s...
0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:2499830"
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35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
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4.2%; Score 35; DB 9; Length 158;

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

DEFINITION

RESULT 11 BI327804

ð g ACCESSION VERSION KEYWORDS

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: University Genome Sequencing Center

cDNA Library MI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.lhl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco

High quality sequence stop: 148.
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Fax: 81-298-36-9098
Email: genome-resourc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases I to 206)
1 (Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Haytawi, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,
Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,
Sato, K., Shibata, Y., Shipamoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N.,
Matranabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
RIKEN Mouse ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B" for cone libe nost="DH10B" for cone libe "NCI CGAP Utl."
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
15 c 45 g 41 t
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="well-differentiated endometrial adenocarcinoma,_7 pooled tumors"
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100.0%; Pred. No. 5.3e-06;
cive 0; Mismatches 0;
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/clone="IMAGE:2212062"
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Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV112006
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ORGANISM
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JOURNAL
COMMENT
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ORIGIN
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AUTHORS
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COMMENT
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AV112006
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       AUTHORS
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KEYWORDS
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/mol_type="mana"
/mol_type="mana"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="taxon:10090"
/clone="tayon:"tayon: policy for the panal for th
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tq48e04.xl NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2212062 3',
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602979552F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5132580 5',
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 162)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapDs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11325 row: g column: 13
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                             Gaps
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Location/Qualifiers
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       Best Local Similarity
Matches 35; Conserv
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FEATURES

AI561355/c DEFINITION

ACCESSION

ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE

BASE COUNT

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Matches

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Gaps 0

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trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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/note="Vector: lambda pSB; Site_1: BamH1; Site_2: EcoR1;
First strand coNA was primed with an anchored
XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGCCGCAGGAGGG(T) VN 3'; V-A, C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer
[5'AGAGAGCTCGGATCGGCGCCGCAATAATAATAAT(C) 3'].
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Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr., Guaratene,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
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1102 Bates, MC3-3320 Houston, TX 77030, USA
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100.0%; Pred. No. 5.4e-06;
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/dev_stage="pediatric 6 years"
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                                                                                                                                                                                                                                                                                                                                                      /dev_stage="10-day embryo"
                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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clone="2610008A07"
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Seg primer: M13 primer.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Eax: 81-45-503-9216
Email: genome-reseggs.riken.go.jp/
URL:http://genome-resegsc.riken.go.jp/
Carnino:,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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E. I. (bases 1 to 239)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagwa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Salinagawa, A., Shizaki, T., Sciabhara, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsundda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB066072 BIKEN full-length enriched, 15 days embryo male testis Mus musculus cDNA clone 8030447L20 3' similar to D17546 Mouse mRNA for
Double-stranded cDNA was then digested with BamH1 and XhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P. Westover A. Nishiyama Y. Ohsumi T., Itoh M. Nagaoka S. SasakiN, Okazaki Y. Muramatsu M. Schneider C. Hayashizaki Y. High efficiency selection of full-length CDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
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100.0%; Pred. No. 5.4e-06;
ive 0; Mismatches 0;
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Contact: Yoghihide Hayashizaki
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/tissue_type="testis"
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       1. .239
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Location/Qualifiers
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Gaps ö Ouery Match 4.2%; Score 35; DB 10; Length 239; Best Local Similarity 100.0%; Pred. No. 5.5e-06; Matches 35; Conservative 0; Mismatches 0; Indels

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204 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 238 795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829 a ò

Search completed: August 17, 2003, 19:46:42 Job time : 2420.32 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Title: Perfect score: 8 Sequence:	US-09-938-391-1 829 1 ccttggcgggcagatgacataataaaaggaagccaaagag,829
Scoring table: (	OLIGO NUC Gapop-60.0 , Gapext 60.0
Searched:	2888711 segs, 20454813386 residues
Word size :	
Total number of }	hits satisfying chosen parameters: 5777422
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Post-processing:	Listing first 45 summaries
Database :	GenEmbl:*  1: gb_ba:*  2: gb_ltg:*  4: gb_om:*  5: gb_ov:*  6: gb_pat:*  7: gb_ph:*  8: gb_ov:*  10: gb_cv:*  11: gb_cv:*  11: gb_cv:*  11: gb_cv:*  11: gb_cv:*  11: gb_cv:*  11: gb_cv:*  12: gb_cv:*  13: gb_un:*  14: gb_vi:*  15: em_fun:*  16: em_fun:*  17: em_fun:*  18: em_fun:*  19: em_ov:*  22: em_ov:*  22: em_ov:*  23: em_pt:*  24: em_pt:*  25: em_fo:*  26: em_ro:*  27: em_fo:*  28: em_htg_nun:*  39: em_htg_other:*  31: em_htg_other:*  33: em_htg_other:*  33: em_htg_other:*  34: em_htg_other:*  35: em_htg_other:*  36: em_htg_other:*  37: em_htg_other:*  38: em_htg_other:*  38: em_htg_other:*  39: em_htg_other:*  40: em_htg_other:*  41: em_htg_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1 AX39629 LOCUS DEFINITION ACCESSION VERSION	AX399629 829 bp D Sequence 1 from Patent EP1191036. AX399629 AX399629.1 GT:21335409	DNA linear	PAT 06-JUN-2002
SOURCE	Canis familiaris Canis familiaris Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.	ta; Vertebrata; pedia; Canidae;	Euteleostomi; Canis.
REFERENCE AUTHORS TITLE	1 Sheppard,M.G. and Tong,X. Methods and compositions for diagnosing and treating disorders involving angiogenesis	ing and treatin	g disorders

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                                       /organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
                                                                                                     100.0%; Score 829; D
100.0%; Pred. No. 0;
ive 0; Mismatches
 Patent: EP 1191036-A 1 27-MAR-2002;
Pfizer Products Inc. (US)
Location/Qualifiers
1. .829
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Matches 829; Conservative
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Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
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ilarity 100.0%; Pred. No. 5.5e-280;
Conservative 0; Mismatches 0;
                                                                                                                                                                          Sheppard, M.G. and Tong, X. Methods and compositions for diagnosing involving angiogenesis Patent: EP 1191036-A 3 27-MAR-2002; Pfizer Products Inc. (US)
 DNA
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/mol_type="genomic DNA"
/db_xref="taxon:9615"
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from Patent W00229103.
555 bp
from Patent EP1191036
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Location/Qualifiers
AX399631
Sequence 3 from Patent I
AX399631
AX399631.1 GI:21335410
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Canis familiaris
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1615 bp mRNA linear ROD 13-AUG-1994
Mus musculus BALB/c alpha 1 type XVIII collagen (COL18A1) mRNA,
partial cds.
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Biochemistry, University of Oulu, Kajaanintie 52 A Fin-90220, Oulu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Termin. V. and Pihlajaniemi, T.

A previously uncharacterized collagen chain, alpha 1(XVIII), with frequent interruptions in the collagenous sequence, a distinct tissue distribution, and homology with type XV collagen Proc. Natl. Acad. Sci. U.S.A. (1994) In press
2. (bases I to 1615)

Rehn, W., Hintikka, E. and Pihlajaniemi, T.
Primary structure of the alpha 1 chain of mouse type XVIII
conlagen, partial structure of the corresponding gene, and comparison of the alpha 1(XVIII) collagen. Chain 1(XVIII)
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mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/dev_stage="adult, 9-10 weeks"
<1. 1449
                                     Hofmann, M., Kaiser, C., Kranz, H., Loebbert, R. and
                                                                                                                                                                                                                                                                             Query Match

4.2%; Score 35; DB 6; Length 338;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 35; Conservative 0; Mismatches 0; Indels
                                                                      Gene library and a method for producing the same
Patent: WO 02074953-A 423 26-SEP-2002;
LION Bioscience AG (DE)
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|Codon start=1
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94245707
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/organism="Mus musculus"
/mol type="mRNA"
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/db xref="taxon:10090"
/sex="male"
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Schlueter, T.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Schlueter,T.
                                                                                                                          Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G. Gene expression profiles in liver cancer Patent: WO 0229103-A 713 11-APR-2002; GENE LOGIC (US)
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                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. AA292773"
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100.0%; Pred. No. 1e-06;
tive 0; Mismatches 0; Indels
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Patent: EP 1236798-A 423 04-SEP-2002;
LION Bioscience AG (DE)
Location/Qualifiers
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Pred. No. 1e-06;
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Sequence 423 from Patent WO02074953.
AX553131
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AX524393
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/db_xref="taxon:10090"
92 c 83 g 9
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 AX408066.1 GI:21440771
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                                     Homo sapiens (human)
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Matches 35; Conserval
                                                    Homo sapiens
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PRI 08-JUL-2002

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 6 Row: e Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R. w., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,N. w., Bouffard,G.G., Breen,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 2637)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (02-UUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                2637 bp mRNA linear PRI 08-JUJ
HOMCO sapiens, Similar to collagen, type XVIII, alpha 1, clone
IMAGE:4425380, mRNA, partial cds.
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/protein id="AAH33715.1"
db_xref="GI:21708149"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                 Length 2364;
                                                                                                                                   Indels
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/tissue_type="Kidney, hypernephroma"
/clone_lib="WIH MGC_89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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                                                                              DB 9; Le
1.1e-06;
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                                                             4.2%; Sco...
100.0%; Pred. No. ...
0, Mismatches
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/db_xref="taxon:9606"
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                                                                              Query Match
Best Local Similarity 100.
Matches 35, Conservative
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Sisogai, T. and Yamamoto, J.

Direct Submission

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Bconomy, Trade and Industry of Japan; ODNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5- & 3-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                              PGAMGASAGQ<sup>®</sup>RIWATYQTMLDKIREVPEGWLIFVAEREELYVRVRNGFRKVLLEART
ALPRCTGNEVAALQPPLVQLHEGSPYTRREYSYSTARPWRADDILANPPRLPDRQPYP
GVPHHISSYHLPPARPTLSLAHTHQDPGPVLHLVALNTPESGGWRGIRGADFQCFQQ
ARAVGLISGTFRAFISSRLQDLYSIVRRADRGSVPITVNLKDEVLSPSWDSLFSGSQQQL
QPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYCETWRTETTGATGQASSL
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highly similar
                                                     translation="DSNAFVESGRPGLPGQQGVQGPSGPKGDKGEVGPPGPPGQFPID
                                                                           LFHLEAEMKGDKGDRGDAGQKGERGEPGAPGGGFFSSSVPGPPGPPGYPG1PGPRGRES
IRGPPGPPGRQGPPGIGYEGRQGPPGPPGPPGPPGPPGPPRFPGPHRQTVSVPGPPGPPGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oshima, A., Takahashi-Pujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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2364 bp mRNA linear
Homo sapiens CDNA FLJ40897 fis, clone UTERU2002964,
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4.2%; Score 35; DB
Best Local Similarity 100.0%; Pred. No. 1.1.
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/clone_lib="UTERU2"
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/db_xref="taxon:9606"
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1584. 1589
/citation=[2]
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CDS
         Submitted (24-NOV-1993) Marko Rehn, University of Oulu, Department of Medical Biochemistry, Kajaanintie 52 A, Oulu, FIN-90220, Finland Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROD 28-MAR-2002
GHKGSKGAPGPAGARGESGLAGAPGPAGPPGPPGPPGPPGLPAGFDDMEGSGGPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rehn, M., Hintikka, E. and Pihlajaniemi, T. Characterization of the mouse gene for the alpha 1 chain of type XVIII collagen (Coll8a1) reveals that the three variant N-terminal polypeptide forms are transcribed from two widely separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 3129)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         יריים אותם 3129 bp DNA linear ROD 28-MAR-20 Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exons 40-43, complete cds.
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/clone_lib="Mouse Cosmid Library in pWE15 by Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rehn, M., Hintikka, E. and Pihlajaniemi, T.

Primary structure of the alpha 1 chain of mouse type XVIII collagen, partial structure of the corresponding gene, and comparison of the alpha 1 (XVIII) chain with its homologue, the
                                                                                                                                                                                                                                                                                                                                         Gaps
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U34608.1:1. .2450,U34609.1:1. .165,U34610.1:1. .3326,
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100.0%; Pred. No. 1.1e-06;
cive 0; Mismatches 0;
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/db_xref="taxon:10090"
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Genomics 32 (3), 436-446 (1996)
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Mus musculus
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(#951303)"
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Best Local Similarity 100.0
Matches 35; Conservative
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MEDLINE
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JUMPAGE 1143. 1857. 34609. 1159. 114 (1346) 11438. 1491, U34608.1143. 1257. 1257. 3257. 34611.11490. 566, U34611.11438. 1491, U34610.112478. 2667, U34611.11590. 1566, U34611.11851. 11037, U34612.11327. 252. U34612.11167. 11829. 11829. 11829. 11839. 11837, U34612.11503. 2534, U34612.11671. 1829, U34612.11503. 25164, U34612.115712. 5774, U34612.115843. 5164, U34612.117451. 5774, U34612.118463. 8552, U34612.118467. 8202, U34612.118463. 8552, U34612.118463. 11847. 11847. 11883. U34612.112083. 11124, U34612.111857. 11883, U34612.112083. 12136, U34612.111097. 11887. 11883, U34612.112083. 12136, U34612.1111857. 11883, U34612.112083. 12136, U34612.1112083. 12136, U34612.1112083. 12136, U34612.111209. 11877. 11883, U0376.112083. 12136, U34613.11187. 11857. 11883, U0376.112083. 12136, U0376.11203. 1223. U03718.11253. 12236, U3716.11203. 1223. U03718.11253. 12236, U3716.11203. 
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U34608.1:43. .587,U34609.1:28. .114,U34610.1:438. .491,
U34608.1:478. .2607,U34611.1:490. .566,U34611.1:851. .1037,
U34612.1:227. .252,U34612.1:994. .1056,U34612.1:1160. .1237,
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U34612.1:6546. .6572,U34612.1:7451. .7486,
U34612.1:6646. .572,U34612.1:8167. .8202,
U34612.1:9667. .9693,U34612.1:10157. .10077,
U34612.1:10667. .9103,U34612.1:1183,
U34612.1:112083. .12136,U34612.1:1183,
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U03716.1.20. .63,U03716.1.408. .536,U03716.1.1029. .1173,

U03716.1.1253. .1326,U03716.1.1601. .1732,U03718.1.262. .294,

96 . .344,942. .1139,1653. .1768,2515. .2728)
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PSPPGPVLYVSVSEDKALVSTPEDERGKPAGAGFGPAGPKGDGGSKGEGQLPGPKGEKG
EPGTIFSPDGAALGPKGAVGFPGFRGPFGPAGFAGFAGFGAGFGBKG
ERGEPGDASLGFSMRGLPGPPGPPGPPGPPKGFPHKGEIGFPGPRPGTNGLKG
EKGEPGDASLGFSMRGLPGPPGPPGPPGPPGMPIYDSNAFVESGRPGLPGQCVQGPS
SQPKGDKGEVCPPGPPGPPIDLFHLEAEMKGDKGDRGDGKGRGEPCBAFPGS
SQPKGDKGEVCPPGPPGPPTDLFFHLEAEMKGDKGDRGDGKGRGEPCAPGGFFPSS
SQPKGDFGCPPGPFGSIRGPPGPPGPPGPPGFPSFPSFP
GPHRQTVSVPGPPGPPGPPGPPGPPGPPGPPGFPSFP
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GGSTTEDPRTEETEEDAAVDSIGAETLPGTGSSGAWDEAIQNPGRGLIKGGMKGGKGE
PGAQGPPGPAGPQGPAGPVVQSPNSQPVPGAQGPPGPQGPPGKDGTPGRDGEPGDPGE
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SGFSGD1ESLRGPRGFPGPPGPPGVPGLPGEPGRFG1NGSYAPGPAGLPGVPGKEGPP
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PVGPPGPPGPPGPPGFAAGFDDMEGSG1PLWTTARSSDGLQGPPGSPGLKGDPGVA
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WRADDILANDPRLDDRQPYPGVPHHASYYNHLPPARPLISAHTHOPDPDVLHIVAL
NTPLSGGRRGIRGADPCCCQARAVGLSGFFRAFLSRLQDLYSIYRAADRGSVPIVN
LKDEVLSPSWDSLFSGSQGQLQDPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLM
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joint(104667.2:345. - 1513, 1034608.1:43. - 587.

1034609.1:28. - 114, 1034610.1:438. - 491, 1034610.1:2478. - 2.

1034611.1:490. - 566, 1034611.1:851. - 1037, 1034612.1:227. . .
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/gene="COL18A1"
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U34612.1:222. .2354,U34612.1:3340. .3366,
U34612.1:5033. .5164,U34612.1:5712. .5774,
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DILANPPRLPDRQPYPGVPHHHSSYVHLPPARPTLSLAHTHQDFQPVLHLVALNTPLS
GERGITGADPPGCFQQARAVGLISGTFRFLSSRLDQDLYSIVRADRGSVPIVMLKDEV
LSPSWDSLFGSQGQLQPQRAF IF SFDGRBVLRHPANPQKSVWHGSPDSGRRLMESYCE
TWRTETTGATQQASSLLGGRLLEQKAASCHNSYIVLCIENSFWTSFSK"
                                      KGEVGPPGPPGPPPIDLFHLEAEMKGDKGDRGDAGQKGERGEPGAPGGGFFSSSVPGP
PGPPGYPGIPGPRGESIRGPPGPPGRQGPPGIGYEGRQGPPGPPGPPGPPRPRQ
                                                                                                         TVSVPGPPGPPGPPGPPGAMGASAGQVRIWATYQTMLDKIREVPBGWLIFVAEREELY
VRVRNGFRKVLLEARTALPRGTGNEVAALQPPLVQLHEGSPYTRREYSYSTARPWRAD
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       GDASLGFSMRGLPGPPGPPGPPGMPIYDSNAFVESGRPGLPGQQGVQGPSGPKGD
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gene expression profiles in liver cancer
Patent: WO 0229103-A 2178 11-APR-2002;
GENE LOGIC INC (US)
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Sequence 2178 from Patent WO0229103.
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Conservative 0; Mismatches
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Sequence 4 from patent US 5643783.
151045.
151045.1 GI:2472748
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/db_xref="taxon:9606"
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Olsen, B.R. and Oh, S.P.
Collagen and uses therefor
Patent: US 5643783-A 4 01-UUL
Location/Qualifiers
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Homo sapiens
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Matches 35; Conserv
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AX409531
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U34612.1:6546. .6572,U34612.1:7451. .7486,

U34612.1:6848. .7909,U34612.1:8167. .8202,

U34612.1:9463. .8552,U34612.1:9134. .9562,

U34612.1:1050. .11124,U34612.1:10105. .10077,

U34612.1:12083. .12136,U34612.1:11857. .11883,

U34612.1:1318. .383,U34612.1:11857. .11883,

U34612.1:1318. .383,U34612.1:1139. .1081,U34613.1:1577. .1639,

U03716.1:25. .1326,U03716.1:408. .536,U03716.1:1029. .1173,

U03716.1:25. .1326,U03716.1:1601. .1722,U03718.1:562. .294,

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U34612.1:2992. .2354,U34612.1:3340. .3366,

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U34612.1:294. .1056,U34612.1:11671. .1829,
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U34612.1:6033. .5164,U34612.1:5712. .5774,
U34612.1:6346. .6572,U34612.1:5712. .5774,
U34612.1:8846. .8552,U34612.1:9534. .9563,
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U34612.1:11050. .11124,U34612.1:11857. .11883,
U34612.1:12083. .12126,U34612.1:12491. .12565,
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U03716.1:1253. .1326,U03716.1:408. .2534,U33718.1:262. .294,
/codon chemical control of the control of 
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ALVYDCEPEPCRVPFPRASQGLIELERGAGLFVGAGTAPADDREQMIESEKVRKTPRV
SPVHGLLDEEDDDEDRASGDFGSGFERSKSHKEDTSLLJGLFQPPPYTSPPLAGGSTT
EDPRTEETEEDAAVDS1GAETLPGTGSSGAWDEA1QNPGRGLIKGGKGGKGEPGAQG
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RSSQQHRHSDVHSD1HGHVPLLPLVTGPLVTASLSVHGLLSVPSSDPSGQLSQVAALP
GFPGTWVSHVAPSSGTGLSNDSALAGNGSLTSTSRCLPLPPTLTLCSRLG1GHFWLPN
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Q1DDPHVGPAY1FGPDSNSGQVAQYHFPKLFFRDFSLLFHVRPATEAAGVLFA1TDAA
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GQGGSPATPAVPIPLVAPAASPDMKEENVAGVGAKILNVAQGIRSFVQLWDEDSTIGH
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protein id="AAC52903.1"
db_xref="G1:1167906"
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CDS

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PAT 07-0CT-1997

linear

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Query Match

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ACCESSION VERSION

HUMCOL18AX

RESULT 12

ORGANISM

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/produc_t="alpha 1(XVIII) collagen"
|produc_t="alpha 1(XVIII) collagen"
|protein id="AAA19787.1"
|db xref="d1:511298"
|translation="ENVAEEVGLLGLGDPLPEKISQIDDPHVGPAYIFGPDSNSGQVATARDAILE TOWNERDFSLLFHVRPATEAAGVLFAILADAQVVVSTGVKTSKDBQQVNISL
LYTEPGASGTQTGASERLPAPROGWHIFFALSOUGGSVALYVDCEEFQRVPFAASQGL
BLERGAGLFVGQAGTADPDFKPQGMISELKVRKTPRVSPVHCLDBEDDDBDRASGDFGS
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GOVGT PGPKGSKGDLGPIGMPGKSGLAGSPGPVGPPGPPGPPGPPGPAGFDDMEG
SGIPLMTTARSSDGLQGPPGPSPGLKGDPGVAGLPGAKGEVGADGAGGIPGPPG
GSPGPKGEKGNPGRENPGKDGVQRPGLPGPCPPGIVIYVSSEDKAIVSTPGPEGKA
GSPGPRGEKGNPGRENPGKGPGCLPGFKGEKGEPGTIFSPDGRRLGHPQKGAKGEPGFR
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GTGSSGAMDDA IQNPGRAFL KGGMKGQKGEPGAQPPGPAGPGPAGPGPVQSSNBQP
VPGAQGPPCPQFEKGTFERNGEFCDPGEBGRPGTTGPQGPPGTPGDVGPKGEKGB
PGIGPRGPPGPPPGPPGPFRQDKLTFIDMEGSGFSGDIESLKGPRĞFPGPPGPPGVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oh,S.P., Kamagata,Y., Muragaki,Y., Timmons,S., Ooshima,A. and Olsen,B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xaa-Yaa repeats identify a distinct family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagenous proteins
Proc. Natl. Acad. Sci. U.S.A. 91 (10), 4229-4233 (1994)
94240111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUSCOLPRO 4031 bp mRNA linea
Mouse alpha 1(XVIII) collagen mRNA, partial cds.
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     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.2%; Score 35; DB 6;
                                                                                                                                                                                               1 (bases 1 to 4031)
Olsen,B.R. and Oh.S.P.
Collagen and uses therefor
Patent: US 5643783-A 1 01-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          720
151044 4031 bp
Sequence 1 from patent US 5643783.
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/db_xref="taxon:10090"
/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
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<1. .3867
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/codon_start=1</pre>
                                                                     I51044.1 GI:2472747
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Matches 35; Conservative
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MUSCOLPRO
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MEDLINE
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GGFFGSSLPGAR-CARAPCT PER PROPEL STROCHED PGGPPGCPPGGTPERCAPEG
GGFPGSSLPGAR-CARAPCT STROCHED PGPPGPPGPPGPGPGGPPGGTPERCAPED
GPPEPPS FPGPHRQT IS VPPGPPGPPGPPGPPGTMGASSGQNRLMATROAMLGQPHEVP
BGWL I PVARQEELLY VRVONGPRKYOLEART PLPRGTDMEVALLQPPVVOLHSDSPY PR
REHPHPTAR PWRADD I LAS PPGL.PEPQPY PGGPHHS SYVHCGPARPTS PPAHSHRDFO
PVHLVALNORLLE PSEMEALF SGSSEGPL KPGAR I SF PDGKDVL RAPPWPOKSVWHGS
PAAVPT VNLLKDELL FPSEMEALF SGSSEGPL KPGAR I SF PDGKDVL RAPPWPOKSVWHGS
DPNGRRI JESY CETWRTEAPS ATGQASSLLGGRLLGQSAASCHHAY I VLCI ENS FWTA
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GOCLADePROPOVYYVSEQDOSVYLVPGPERGREGPAGPFAGPKGLGSKGELGS
PGPKGEKGEPGSIFFSPDGGALGPAQKGAKGEPGFRGPPGLYGRPGYKGEIGPERRPG
PGPKGEKGEPGDASLGFGMRGMPGPPGPPGPPGPPGTPVYDSNVPAESSRPGPPG
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                                                                                                                                                                                                                                                                     HUMCOLIBAX 3394 bp mRNA linear PRI 01-NOV-1994 Human collagen type XVIII alpha 1 (COLIBA1) mRNA, partial cds. L22548
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1 (bases 1 to 3394)

Oh, S.P., Warman, M.L., Seldin, M.F., Cheng, S.D., Knoll, J.H.,

Timmons, S. and Olsen, B.R.

Cloning of cDNA and genomic DNA encoding human type XVIII collagen and localization of the alpha 1(XVIII) collagen gene to mouse chromosome 10 and human chromosome 21

Genomics 19 (3), 494-499 (1994)
                                                   Gaps
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Score 35; DB 6; Length 3394;
Pred. No. 1.1e-06;
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                                              Indels
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Location/Qualifiers
1. .3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="collagen type XVIII alpha 1"
/protein_id="AAA51864.1"
/db_xref="G1:562794"
                                                                                                                               2187 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 2221
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100.0%; Pred. No. 1.1e-06;
iive 0; Mismatches 0;
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               100.0%; Prec. ...
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/dev_stage="adult"
1. .3394
                                                                                                                                                                                                                                                                                                                                                                     alpha-1 type XVIII collagen.
Homo sapiens (human)
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  4.2%;
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Best Local Similarity 100.
Matches 35, Conservative
                                                 Conservative
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                       Best Local Similarity
Matches 35; Conserv
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BASE COUNT ORIGIN

RESULT 13 151044

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Indels

Length 4031;

ROD 18-JUL-1994

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GPRGMPIYDSNAFVESGREGLEGGQGVQGPSGPKGDKGEVGPPGPPGDFPDLFHLEA
EMKGDKGDRGDAGQKGREGEPGAPGGFPSSSYPGPPGPPGYEGIPGESIRGPEG
PPGPQGPPGIGYEGRQGPPGPPGPPSFSSYPGPPGPPGPPGPFGPRGAMGA
SAGOVHLWATYOOTHLDKIREVEPGWLIFVABERELYWRYNGFRKVLLEARTALLRGT
GNEVAAPQPPLVQLHEGSPYTRREYSYSTARPWRADDILANPPRLPDRQPYPGVPHH
SGYTHLPPRAPTISLAHTHQDRQPVLHHVALMYPPLSGGMRGIRGADFGCFQQARAVGL
SGTFRAFLSSRLQDLYSIVRRADRGSVPIVNLKDEVLSPSWDSLFSGSQGQVQPGARI
FSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYCETWRTETTGATGGASSLLSGRLL
EQKAASCHNSYIVLCIENSFWISFSK"
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TPRVSPVHCLDEEDDDEDRASGDFGSGFEESSKSHKEDTSLLPGLPQPPPVTSPPLAG
GSTTEDPRTEETEEDAAVDSIGAETLPGTGSSGAWDEAIQNPGRGLIKGGMKGQKGEP
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RODKGEVGPGPDGPPGQPFIDLFHLLERHKGDKGDDGAGKGRERGERGARGGGFRSSS
VGCPPGPPGYPGIPGGSIRGPPGPPGPGPPGPGPFIGYBGRQGPPGPPSFPSFPSPPFPPG
PHRQTVSVPGPPGPPGPPGPPGAMGASAGQVRIWATYQTMLDKIREVPEGWLIFVAER
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GFSGDIESLRGPRGFPGPPGPPGVPGLPGEPGRFGINGSYAPGPAGLPGVPGKEGPPG
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Abe, N., Muragaki, Y., Yoshioka, H., Inoue, H. and Ninomiya, Y. Identification of a novel collagen chain represented by extensive interruptions in the triple-helical region
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Submitted (04-SER-1993) Nobuhiro Abe, Okayama University Medical
Submitted (04-SER-1993) Nobuhiro Abe, Okayama University Medical
School, Molecular Biology and Biochemistry; 2-5-1, Shikata-cho,
Okayama, Okayama 700, Japan (Tel:81-86-223-7151(ex.2390),
Fax:81-86-222-7768)
On Jun 5, 1997 this sequence version replaced gi:467516.
Location/Qualifiers
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4.2%; Score 35; DB 10; Length 4031;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0
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D17546
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/organism="Mus musculus"
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Mus musculus
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VERSION
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AUTHORS
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EELYVRVRNGFRKVLLEARTALPRGTGNEVAALQPPLVQLHEGSPYTRREYSYSTARP
                  WRADDILANPPRLPDRQPYPGVPHHHSSYVHLPPARPTISLAHTHQDPQPVLHLVALN
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KDEVLSPSWDSLFSGSGGGLGGARI FSFDGRBVLAHPAWPQKSVWHGSDPSGRRLME
SYCETWRTETTGATGQASSLLSGRLLEQKAASCHNSYIVLCIENSFWTSFSK"
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100.0%; Pred. No. 1.1e-06;
iive 0; Mismatches 0;
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                                                                                                                    /evidence=experimental
3558. .3563
/evidence=experimental
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Matches 35; Conservative
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ò В Search completed: August 17, 2003, 18:39:17 Job time : 4164.77 secs

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Human ovarian anti
Human alpha-1 coll
Human alpha-1 coll
Human alpha-1 (XVII
Gene #2178 used to
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Canine angiogenesi
                                                                                                                                                  August 17, 2003, 12:12:16 ; Search time 319.261 Seconds (without alignments) 7009.423 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                      1 ccctggcgggcagatgacat......aataaaaggaagccaaagag 829
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
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| SIDS1/gcgdata/geneseq/geneseq-embl/NA1983.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:
/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:
/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2552756 seqs, 1349719017 residues
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Listing first 45 summaries
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AAX78379
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                                                                                                   OM nucleic - nucleic search, using sw model
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0 0 0	Human endostatin D Human angiogenesis Human angiogenesis Human gene fragmen Human endostatin c SEQ ID 50 of W0991 Nucleotide sequenc Human endostatin c Human endostatin c Human endostatin c	Human endostatin e Specific tumour ce Reproductive recom Anticancer gene-as Human endostatin c Nucleotide sequenc Alternate human en Human gene fragmen Syntheric plasmid	Human endostatin c Murine endostatin CDNA encoding mous DNA encoding anti- Mouse endostatin c Mouse endostatin e Rat endostatin e
	v		
ABK09977 ABV94763 ABV94763 ABV85301 AAC62025 ABQ76740 AAT84485 AAA64013 AAA64013 AAA69013 AAA99261 AAA99261 AAA204	AAX77719 AAA29884 AAZ51291 AAS00867 ABA00774 AAX35375 AAC62023 AAG62023 AAG6203	AAH79104 AAL55454 AAL44000 ABQ76079 ABQ76079 AAA64014 AAA64014 AAA27005	AZ50378 AAZ50398 AAZ50398 AAZ58740 AAX58740 AAZ08748 AAD18701 ABQ76173
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## ALIGNMENTS

AAL46062 standard; cDNA; 829 BP.

RESULT 1 AAL46062

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ischaemic limb angiogenesis, diabetic neovascularisation, fracture, cytostatic, antiarthritic, antipsoriatic, antidiabetic, ophthalmological,
                                                                                           Dog; pro-endostatin; endostatin, angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral;
                                                                                                                                                                                               cerebral collateral; arteriovenous malformation;
                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "pro-endostatin"
/partial
                                                                                                                                                                                                                                                                                                                                                                                             /note= "no start codon"
                                                              Canine pro-endostatin coding sequence.
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                              (first entry)
                                                                                                                                                                                                                                             gynaecological; gene; ss
                                                                                                                                                                                                                                                                                                                                . 693
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                              19-JUL-2002
AAL46062;
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EP1191036-A2

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ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psortasis; kremmatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; collateral; arteriovenous malformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated nucleic acid molecule for the treatment of angiogenesis-related disorder, such as cancers or diabetic retinopathy, encodes an endostatin protein -
                    541 TGGGAGACGTGGACGGCCCCGGCCGCCACCGGCGAGGCGTCGTCGTGGCG
                                                                                                                                                                        GAGGGGCCCCCCCCAGGAGCATCCGCCCCCGGGGGGGCCTGGCCGGGGACGCTTGCCTG
TGCGAGACGTGGCGGACGGACGGACGCCCCCGGCCACCGGGCAGGCGTCGTCGCTGCTGCTGCTGGCG
                                                                                                           GGCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC
                                                                                                                                              GAGGGGGCGCCCGCAGGAGCATCCGCCGCCCCGGGGGGGCCTGGCCGGGACGCTTGCCTG
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/partial
/note= "no start codon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canine endostatin coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-AUG-2000; 2000US-227924P.
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                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatchd arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, mycardial angiogenesis, plaque neovascularisation, telanglectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, neatformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine pro-endostatin coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                 An isolated nucleic acid molecule for the treatment of angiogenesis-related disorder, such as cancers or diabetic retinopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCCGCGCCTGCTGGACCCCCCAGCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAACAGCCCGCAGCCGGGCGGCATGCGAGGCATCCGGGGAGCGGGACTTCCAGTGCTTC
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 829 BP; 124 A; 314 C; 278 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                       encodes an endostatin protein
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                                                                      2000US-227924P
                                   24-AUG-2001; 2001EP-0307224
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ses 829; Conservative
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                                                                                                        (PFIZ ) PFIZER PROD
                                                                                                                                                                              WPI; 2002-354068/39.
P-PSDB; AAO17429.
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27-MAR-2002
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metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retrinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy; ds.

/product= "Endostatin"
/note= "Does not include stop codon"

/partial

WO200011033-A2

98US-0097883

25-AUG-1998; 25-AUG-1999; 02-MAR-2000

(LEXI-) LEXINGEN PHARM CORP

Li Y, Gillies

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WPI; 2000-237616/20.

P-PSDB; AAY70265

Location/Qualifiers

Canis familiaris.

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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque meovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound gramulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
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Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -

Example 8; Pages 58-59; 68pp; English.

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The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis confinibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including conditions, accoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases c. g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis and osler-webber syndrome; mycocardial angiogenesis, plaque neovascularisation, telangiectasia, heemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and chypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encoding canine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 552 BP; 77 A; 204 C; 190 G; 81 T; 0 other;
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GTGCGCCGGCCGACCGCACCGCGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTTTC
                                                                                                                     TTCTCTTTCGACGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGAGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ovarian antigen HEEBK29 cDNA, SEQ ID NO:835.
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to compinant vectors and host cells comprising human ovarian antigens of polynucleotides and polypeptides in diagnosing, reproductive spatem of ovarian antigens of ovarian or breast corgin, reproductive system of isorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasamosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and capired wagnitis), immune disorders (e.g., congenital and acquired immunedeficiencies, autoimmune oophoritis, systemic lupus erythematosus), clood-related disorders (e.g., anaemia), cardiovascular disorders, crepiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypetides and companial comp
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at ftp.wipo.int/pub/published_pct_sequences.
                                       Claim 1; SEQ ID No 835; 2922pp; English
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                                                                                                                                          Score 503.2; DB 20; Length
Pred. No. 3.4e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasminogen, human, angiostatin, endostatin, gene therapy, collagen 18, anti-angiogenic, attenuation, cytostatic, anti-diabetic, ophthalmology, tumour growth, solid tumour, diabetic retinopathy, retina, vector, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiostatin, human or murine endostatin and angiogenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vecto expresses an anti-angiogenic polypeptide. An additional use comprises
                                                                                                                   2914 TGTGAGACGTGGGGGACGGAGGCTCCCTCGGCCACGGCCAGGCCTCCTCGCTGCTGGG
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MASSACHUSETTS INST TECHNOLOGY
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                                                                                                                                                                                                     1906 TGTGAGACGTGGCGGACGGAGGCTCCCTCGGCCACGGCCTCCTCGCTGGGG
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    "Partial sequence, no start codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen (AAW26327) that is expressed in multiple tissues, especially liver, lung and kidney. It was isolated from a placental cDNA library using a probe based on an unidentified collagenous protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A cDNA clone (AAT84484) codes for a human novel type alpha-1 (XVIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and a probe based on mouse alpha-1 cDNA clone mc19. A claimed plasmid comprising alpha-1 collagen nucleic acid and an expression control sequence can be used to express recombinant collagen in prokaryotic or eukaryotic (especially mammalian) host cells. The collagen may be used to treat a patient suffering from a disease
                                                                                                                                                                                                                           ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen may be used to treat a patient suffering from a disease associated with degradation of cartilage, and for supplementing
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                                                                                                                                                                                                                Alpha-1 collagen; type XVIII collagen; cartilage degeneration;
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0; Mismatches 157; Indels
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larity 77.1%; Pred. No. 3.9e-73;
Conservative 0; Mismatches 157;
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/*tag= a
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     CDNA; 3394
                                                                                                                                                                  Human alpha-1 collagen cDNA.
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P-PSDB; AAW26327.
     AAT84484 standard;
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                                                                                                                                                                                This invention describes a novel method for identifying mimetics of mammalian endostatin. The method comprises identifying a compound having atomic coordinates with non-trivial similarity to selected coordinates of atoms of a mammalian endostatin involves (a) providing a library of atomic coordinates of compounds in a library of candidate compounds, (b) comparing the library of atomic coordinates of the intervent of atomic coordinates of a mammalian endostatin and (c) selecting from the library at least one candidate compound on the basis of selection criteria which include similarities between the atomic coordinates of the selection candidate compound and the atomic coordinates of the mammalian
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                                                                                                                                                                                                                                                                                                                                         endostatin. The invention also describes the use of an anti-angiogenic fragment of endostatin comprising a domain selected from a heparin binding domain, and exposed on alpha-helix A domain, and a carbohydrate recognition domain (CRD) domain. The methods identified can be used for treating endostatin mimics. The compounds fidentified can be used for treating undesired anglogenesis, e.g. tumours. This sequence encodes human alphal(XVIII) collagen which is used in the description of the method.
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                                                                                                                       Identifying mimetics of mammalian endostatin
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                                                                                                                                                     Disclosure; Fig 5A-C; 75pp; English
                                           Sasaki T,
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              (HARD ) HARVARD COLLEGE
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                                           Hohenester E,
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disease progression; drug toxicity; drug efficacy; drug metabolism
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                                                                                                                                                                              CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCCGGCGCCTGCTGGACCCCCAGCCCTAC
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                            Length 3394;
                                                                                                                                             39;
                                                                                                            Query Match 59.9%; Score 496.8; DB 24; Length Best Local Similarity 77.1%; Pred. No. 3.9e-73; Matches 660; Conservative 0; Mismatches 157; Indels
                                                                                Seguence 3394 BP; 668 A; 1130 C; 1080 G; 516 T; 0 other;
drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
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σ RESULT

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Producing functional protein domain by growing host cell transfected with DNA construct having regulatory DNA and DNA targeting segment, and optionally culturing homologously recombinant cell and collecting
                                                                        Mouse; Ig signal peptide; mIgSP; functional protein domain; FPD; primary translational product; PTP; DNA construct; regulatory DNA; DNA targeting segment; regulatory factor; single regulatory unit; monoclonal antibody; recombination-derived alteration; blood product;
                                                                                                                                                                                                          exon"
                                                                                                                                                                                                                                                                                           protein exons 38-41"
                                                                                                                                                                                                                                                               "(MIgSP)"
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number= 1
'note= "Mouse Ig signal peptide (mIgSP)
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                                                     Synthetic plasmid pEnd-HR#1 FPD fusion DNA sequence.
                                                                                                             human; COL18A1; gene; mutant; fusion protein; ds
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note= "Mouse Ig signal peptide
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note= "Human COL18A1
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such as functional protein domain, that is either C- or N-terminus of the primary translational product (PTP) of a gene, where the protein has biological activity which is distinct from PTP. The method of the invention involves growing a host cell transfected with a DNA construct comprising a regulatory DNA and a DNA targeting segment. This method is useful for producing a functional protein domain of proteins such as cagnatory factors, blood products and monoclonal antibodies. The method described in the invention allows controlled and precise modification of the host cell genome in order to produce functional protein domain (PPD). The amount of exogenous sequence to be integrated in the host cell genome is ording sequence, the original coding sequence present in the host cell genome itself is used. Use of the host cell sequence accoding PPD also provides the advantages of both eliminating any recombination-derived alteration of such coding sequence, and also making use of the same post-transcriptional (e.g., splicing) and/or post-translational (e.g. glycosylation, phosphorylation) processes that streatly applied in vivo for the maturation of FPD. The use of a single regulatory unit eliminates the necessity of manipulating the complementary DNA coding for the PPT to isolate the segment coding for the PPD, and adapt it to the expression vector. The present undleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nvention. The FPD fusion protein contains the mouse Ig signal peptide
present invention relates to a new method of producing a protein,
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Sequence 900 BP; 146 A; 336 C; 274 G; 144 T; 0 other;

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                                                                             CCCTGGCGGCCAGATGACATCCTGGCCGGCCCCCCCGCGCCTGGTGGACCCCCAGCCCTAC
                                          Gaps
                                        12;
   DB 24; Length 900;
Score 493.2; DB 24; Length
Pred. No. 1.7e-72;
0; Mismatches 98; Indels
   59.5%;
83.9%;
                   Best Local Similarity 83.9
Matches 574; Conservative
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799 GGCAGGCTCCTGGGGCAGAGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATT 858
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                                                                                                                                                               cancer; gene therapy; vaccine; immunostimulant;
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for diagnosing, preventing and/or treating cancer, particularly
                                                                                                                                                                                                                                                                                                                                                                                         Persing DH, Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 144; 300pp + Sequence Listing; English.
                                                                                                                                           Human pancreatic cancer expressed cDNA SEQ ID NO 144.
                                     859 GAGAACAGCTTCATGACTGCCTCC 882
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                  GAGAACAGCGTCATGACCTCCTTC
                                                                                   BP.
                                                                                   ABV94763 standard; cDNA; 4551
                                                                                                                                                                        cytostatic; tumour; gene; ss.
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12-JUL-2001; 2001US-305484P.
20-AUG-2001; 2001US-313999P.
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2001US-267568P
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                                                                                                                                                                                                              WO200260317-A2.
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
(b) complements of (a), (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences that hybridize to (a), under identity to (a); or (f) degenerate variants of (a). Polypeptides (a), or (f) degenerate variants of (a). Polypeptides (a), or (f) degenerate variants of (a). Polypeptides (a) polymcleotides, netibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polymucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. printed om WIPO Note: The sequence data for this patent did not form part of the pr specification, but was obtained in electronic format directly from

Sequence 4551 BP; 780 A; 1597 C; 1522 G; 652 T; 0 other;

ftp.wipo.int/pub/published\_pct\_sequences.

Query Match

DB 24; Length 4551; 59.5%; Score 493.2;

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CCCCAGAAGAGGGTGTGGCATGGCTCGGACCCCAACGGGCGCAGGCTGACCGAGAGCTAC
                                                                                   Kim S;
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83.9%;
                                              05-JAN-2001; 2001KR-0000691.
                            03-JAN-2002; 2002WO-KR00001
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Matches 574; Conservative
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                                                                (VIRO-) VIROMED LTD
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                                                                                                                                                                                        comprising a DNA encoding an anti-angiogenic protein, which shows therapeutic effects on rheumatoid arthritis. The composition is useful for treating rheumatoid arthritis and the gene therapy is effective, lasting for 14 days. The present sequence is the coding sequence for human collagen XVIII. Endostatin, which consists of the C-terminal 183 residues of collagen XVIII, was used as an anti-angiogenic protein.
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Novel composition for gene therapy against rheumatoid arthritis, comprising a DNA encoding anti-angiogenic protein or its parts
                                                                                                                                                             The present invention relates to a composition for gene therapy
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Pred. No. 1.5e-72;
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                                                                                             Disclosure; Page 60-70; 84pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparation of soluble recombinant endostatin involves transforming Streptomycete host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader
                                                                                                                                                                                                                                                                                                                              sequence of vaa-endostatin fusion protein in pANT3052
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endostatin; cancer; tumour growth; anglogenesis; ss.
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receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced.
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vascular endothelial cytopoiesis inhibiting factor; inhibitor;
fusion construct; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 CGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCAGGCGGCATGCGGGGCATCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCGGACTTCCAGTGCTTCCAGCAGGCGCGCGCGCGGGGGCTGGCCGGCACCTTCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATCGTGCGCCGCCGCCGACCGCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATCTTCTTTTCGACGCCAGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCGTCGTCGCTGCTGCCGGCCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     859 AGGCCTCCTCGCTGCTGGGGGGCAGGCTCCTGGGGCAGAGTGCCGCGAGCTGCCATCACG
                                                                                                                                                                                                                                                                                                                                                                                   379 cedecaacecccedcecadeccarccccccedaarcccacaccaccecaacrrccaec
                                                                                                                                                                                                                                                                                                                                                                                                                                        161 TGGTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCGGGCGGCATGCGAGGCATCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 679 CAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCCACGCATCTTCTCCTTTGACGGCAAGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGCCTGACCGACAGCTACTGCGAGACGTGGCGGAGGCCCCCGGCGCCCACCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 GGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTCCCCCAGCTGGGAGGCCTTATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        739 recrigadecaceceaecredececeaaaaaaagegreregeargeeregaacecaaegee
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                    DB 21; Length 968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               919 CCTACATCGTGCTCTGCATTGAGAACAGCTTCATGACTGCCTCC 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACCTCCTTC 684
                                                                                                                                                                                                                                                                                    99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding human Endostatin/IgG1Fc fusion construct
                                                                                                                                                                                 Sequence 968 BP; 153 A; 335 C; 331 G; 149 T; 0 other;
                                                                                                                                                                                                                              Score 425.6; DB 2
Pred. No. 2.1e-61;
                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..1527
                                                                                                                                                                                                                                    51.3%;
83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ76740 standard; DNA; 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                    al Similarity
485; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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799

796

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740 AGAGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATTGAGAACAGCTTCATGA
                                                                                              800 creccircaagragradrade-----agaaagcggaggregagggregacaa
                                                                                                                                                                             737 GAGCATCCGCCCCCGGGGGGCCTGGCCGGGACGCTTGCCTGCACCGTCACGTTTAAT
                                                                                                                                                                                                            849 AACTCACACATGCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCT
                17 AGGAGGCCGCGCGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A cDNA clone (AAT84485) codes for a mouse novel type alpha-1 (XVIII) collagen (AAW26328) that is expressed in multiple organs, especially the liver, lung and kidney. It was isolated by screening murine 15.5- and 17.5-day embryo libraries with probes based on murine nucleic acids can be used to express recombinant alpha-1 solated nucleic acids can be used to express recombinant alpha-1 collagen in transformed host cells. Claimed nucleic acid (see AAT84484) coding for human alpha-1 collagen (and iseases associated with degradation of cartilage, and for supplementing collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-1 collagen; type XVIII collagen; cartilage degeneration; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4031 BP; 873 A; 1172 C; 1266 G; 720 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 423; DB 18; 1 Pred. No. 4.9e-61; 0; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..3867
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 2; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                          797 GTAATCCTCAAGAAATAA 814
                                                                                                                                                                                                                                                                                              909 crrccccchhaacccah 926
                                                                                                                                                                                                                                                                                                                                                                                                  AAT84485 standard; cDNA; 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.0%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse alpha-1 collagen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0159784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0159784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 76.9
Matches 548; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-350247/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olsen BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW26328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5643783-A
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT84485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SP,
                                                                                                                                                                                                                                                                                                                                                         RESULT 14
AAT84485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for the preparation of recombinant human vascular endothelial cytopolesis inhibiting factor with human IgGIPc fragment molecular structure and its product application. The novel factor is derived from endostatin (using PCR to screen a human foetal kidney cell CDNA library) and human IgGIPc. The product of the invention can specifically inhibit tumour vascular endothelial proliferation and can be used for curing several tumour types. This sequence encodes a fusion construct composed of human endostatin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCACAGCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rececricececcierrecececerrecrerececerececerecres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCACGCA ,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTCTCTTTCGACGGCAGAGAIGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTCTCTTTGACGGCAAGGACGTCCTGAGGCACCCCACACGCCCCAGAAGAGCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCACACCACCAGGACTTCCAGCTGGTGCTGCAGCTGGTGGCCCTGAACAGCCCGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGCGGCATGCGGGGCATCCGCGGGGCCGACTTCCAGTGCTTCCAGCAGCGCGGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGGGCTGGCCGGCCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGTGCGCCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rcerececereceaececeaecerecearecereaecereaecereaecereae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGAGGCCCCGGCCACCGGCCAGGCGTCGTCGCTGCTGGCGGGCAGGCTGCTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                Preparation of recombinant human vascular endothelial cytopoiesis suppressor factor with human LgG1Fc fragment molecular structure and application of its product -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Length 1564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human IqG1Fc, described in the disclosure of the invention
                                   /transl_except= (pos58..60,aa:Ala)
/transl_except= (pos:811..816,aa:GGGGSGG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 423.6; DB 24; Length
Pred. No. 4.2e-61;
0; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1564 BP; 346 A; 491 C; 436 G; 291 T; 0 other;
                                                                                                                                                                                                                                                             (LIAO-) LIAONING WEIXING BIOLOGICAL PROD INST CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 7-8 (Disclosure); 12pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.18;
77.98;
                                                                                                                                                                             30-NOV-2000; 2000CN-0123347.
                                                                                                                                                                                                                     2000CN-0123347
/*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                  Liu Q;
                                                                                                                                                                                                                                                                                                                                        2002-751441/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABG73586
                                                                                                                                                                                                                                                                                                Li Z,
                                                                                                                                                                                                                     30-NOV-2000;
                                                                                                CN1354186-A
                                                                                                                                       19-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557
                                                                                                                                                                                                                                                                                                  Chen L,
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GCGTGTGGCATGGCTCGGACCCCAACGGGCGCAGGCTGACCGAGAGCTACTGTGAGACGT, 616
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                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a human polypeptide which is a potent angiogenesis inhibitor, designated KED. The KED polypeptide, kringle proteins, or a kringle derived from human tissue plasminogen activator (tPA) protein are used to inhibit angiogenesis. Kringle protein, KED or tPA are useful for treating tumours, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCATCGTGCGCCGCCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 ACAGCATCGTGCGCCGTGCCGACCGCGCGCGTGCCCATCGTCAACCTCAAGGACGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTGTTTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCACACCCACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCCCTGAACAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACGCATCTTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCCACCTGGCCCCAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGTGTGGCCACGGCTCCCAACCCCAGCGCCCCCTGACCGACAGCTACTGCGAGACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTGTCAGGCGGCATGCGGGGCATCCGCGGGCCGACTTCCAGTGCTTCCAGCAGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCGCATCTTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGGCCTGGCCCCGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cccanangcacacaccaccactriccasccosticcacciccaccinegricoscicaacacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCAGCCGGGCGGCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTCCAGCAGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u> GCGCCGCGGGGTGGCCGGCACTTCCGGGCCTTCCTGTCGTCGCGCGGCTGCAGGACCTCT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGCGTGGGGCTGGCGCTTCCGCGCTTCCTGTCCTCGCGCCTGCAGGACCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory bowel disease, adult respiratory distress syndrome, Castleman's disease, psoriasis, hepatitis, aneurysm, renal disease
                                                                                                                                                                                                                                                                                Use of kringle protein and kringle derived from plasminogen and composition comprising kringle proteins for treating tumor and atherosclerosis, arthritis and retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 816 BP; 156 A; 259 C; 254 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 421.2;
Pred. No. 1.1
                                                                                                                                                                                                 Ë
                                                                                                                                                                                               Mikkelsen
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 151; 163pp; English
                                                                                                                                                                (FORD-) FORD HEALTH SYSTEM HENRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.0%;
                                                                                                               99US-0121633.
99US-0166176.
                                                                2000WO-US04798
                                                                                                                                                                                               Wang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                  2000-572016/53
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les 471; Conserv
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Search completed: August 17, 2003, 13:19:25 Job time : 324.261 secs

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ABV94691 **ABV94763** 

ABN8530

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immune/haema Human immune/haema Murine collagen XV

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ALIGNMENTS

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ABQ81193 AAC62023

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Human angiogenesis

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ischaemic limb angiogenesis, diabetic neovascularisation, fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological;
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Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; plaque neovascularisation; coronary collateral; cerebral collateral; arteriovenous malformation; cerebral collateral; arteriovenous malformation; schaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiathritic; antipsoriatic; antidiabetic; ophthalmological;
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rheumatoid arthritis;

psoriasis;

atherosclerosis;

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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
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                                                                                    rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
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Canine; immunoglobulin Fc fragment; endostatin; immunofusin; angiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; immunosuppressant; asotropic; vulnerary; treatment; antiarteriosclerosis; tumour;

Canine angiogenesis inhibitor, endostatin DNA

(first entry)

06-JUN-2000

AAZ51309;

BP.

AAZ51309 standard; DNA; 552

RESULT 3

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a signal sequence, an immunoglobulin Fc region, an anglogenesis including a gignal sequence, an immunoglobulin Fc region, and an anglogenesis inhibitor selected from anglostatin, endostatin, a plasminogen fragment having anglostatin activity, a collagen XVII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit anglogenesis and to treat diseases or conditions mediated by anglogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign trachomas and pyrogenic reamanglomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, coular anglogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental confibroma, wound granulation, telangiectasia, haemophiliac joints, anglodibroma, wound granulation, telangiectasia, haemophiliac joints, endostand granulation, and excessive or abnormal stimulation of hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encoding canine immunolominic containing canine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a DNA molecule encoding a fusion protein comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis,
               ocular angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 GGTGCTGCACCTGGTGGCCCCTGAACAGCCCGCAGCCGGGCGGCATGCGAGGCATCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 GGTGCTGCACCTGGTGGCCCTGAACAGCCGCAGCCGGGCGGCGCATGCGAGGCATCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 CTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATCGTGCGCCGCCGCCGACCGCACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 AGCGGACTTCCAGTGCTTCCAGCAGCGCGCGCGCGGGGCTGGCCGGCACCTTCCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such as rheumatoid arthritis, tumors and macular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 552;
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/ttag=
/ttag=
/roduct= "Endostatin"
/note= "Does not include stop codon"
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                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmunoglobulin Fc fragment
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Matches 529; Conservative
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                                                                                       Canis familiaris.
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                                                                                                                                                                                                                                                                                                                                 25-AUG-1999;
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                 GGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTC
                                                                           GGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATCTTCTTTTCGACGCCAGAGATGT
                                                                                                                     CCTGCAGCACCCCGCCTGGCCCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAACGGGCG
                                                                                                                                        CCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGGCG
                                                                                                                                                                                CGCCTGACCGACAGCTACTGCGAGACGTGGGCGGACGGAGGCCCCGGCGGCCACCGGGCCA
                                                                                                                                                                                                                                          GECGTCGTCGCTGCCGCGCCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCCACGC
                                                                                                                                                                                                                                                                      GGCGTCGTCGCTGCTGGCGGGCAGGCTGCTGGAGCAGGAGGCCGCGAGGTGCCGCCACGC
GGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTCCCCCAGCTGGGAGGCCTTATTCTC
                                                         GGGCTCCGAGGCCAGCTGAAGCCCGGGGCCCGCATCTTCTCTTTCGACGGCAGAGGTGT
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AAL46065 standard; DNA; 35

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AAL46065;

(first entry) 19-JUL-2002 Murine collagen XVIII PCR primer used to amplify canine collagen cDNA #1.

cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological; mouse; collagen XVIII; PCR; primer; ss. Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rhemmatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler Webber Syndome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; plaque neovascularisation; telangiectasia; haemophiliac joints; erebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; 

EP1191036-A2

27-MAR-2002.

24-AUG-2001; 2001EP-0307224

25-AUG-2000; 2000US-227924P.

(PFIZ ) PFIZER PROD INC.

Tong X; Sheppard MG,

WPI; 2002-354068/39.

An isolated nucleic acid molecule for the treatment of angiogenesis-related disorder, such as cancers or diabetic retinopathy. 36; 56pp; English. encodes an endostatin protein -Examples; Page

The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration,

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                                                                                                                                                                                                                                                                                                                                                      primer
corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial anapiogenesis, plaque neovascularisation, telangiectesia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is a PCR primer derived from murine collagon XVIII CDNA and used to amplify the canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35 BP; 5 A; 7 C; 5 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.2%; bcc. 100.0%; Pred. No. ... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen XVIII cDNA
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Best Local Similarity
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ABN94215/
              8 \times 8 
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Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism. 02-OCT-2001; 2001WO-US30589 02-OCT-2000; 2000US-237054P (GENE-) GENE LOGIC INC. WO200229103-A2 Homo sapiens. 

state;

Gene #713 used to diagnose liver cancer.

(first entry)

13-AUG-2002 ABN94215;

Vockley JG; Peres-Da-Silva S, Alvares C, Horne D,

WPI; 2002-426119/45.

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in tissue sample liver

Claim 1; SEQ ID NO 713; 298pp; English.

progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN9455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, The invention relates to a novel method for diagnosing and detecting the printed drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the pr
specification, but was obtained in electronic format directly from
at ftp.wipo.int/pub/published not seminance ftp.wipo.int/pub/published\_pct\_sequences. S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine transport and binding associated protein encoding cDNA SEQ ID 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences with specific 3'-ends and no polyA involved in a wide range of cellular processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell metabolism, energy metabolism; fatty acid metabolism; synthesis; phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide; replication; transport protein; ss.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine; liver; gene library; amino acid synthesis; binding protein;
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                                                                   24; Length 251;
                                                                                                                                              0; Indels
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Sequence 251 BP; 44 A; 72 C; 75 G; 60 T; 0 other;
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                                                                                                                                                                                                                  795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829
                                                                   Score 35; DB 24;
Pred. No. 4e-06;
                                                                                                                                                                                                                                                       41 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 7
                                                               Claim 15; Page 134; 251pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                    858/c
AAK53858 standard; cDNA; 338 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                              35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene library containing tail, encoding proteins
                                                                       Query Match
Best Local Similarity
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AXX Murin

EDB Murin

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(first entry) 22-AUG-2002

Human ovarian antigen HODFU24 cDNA, SEQ ID NO:1465.

ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss. ovarian antigen; ovary; ovarian; breast; cancer; tumour;

Homo sapiens.

WO200200677-A1.

3-JAN-2002

07-JUN-2001; 2001WO-US18569.

07-JUN-2000; 2000US-209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

2002-147878/19. P-PSDB; ABP42508 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases

Claim 1; SEQ ID No 1465; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABG54131-ABG5305), and also encompasses polypeptides 90% identical and polyuacleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens of polyuacleotides, antibodies against human ovarian antigens, and the use of ovarian antigens, antibodies against human ovarian antigens, and the use of ovarian antigens, and preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, oplycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastltis, ophoritis and immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, espiratory disorders (e.g., anaemia), cardiovascular disorders, espiratory disorders (e.g., anaemia), cardiovascular disorders, espiratory disorders (e.g., anaemia), cardiovascular disorders) and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the

sequence data for this patent did not form part of the printed tion, but was obtained in electronic format directly from WIPO specification, but was obtained in electroni at ftp.wipo.int/pub/published\_pct\_sequences.

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Gaps

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0; Indels

0; Mismatches

100.08;

35; Conservative

Matches

Query Match Best Local Similarity

795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829

ATGTAATCCTCAAGAATAAAAGGAAGCCAAAGAG 5

39

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Score 35; DB 22; Length 338; Pred. No. 4e-06;

Sequence 697 BP; 173 A; 205 C; 184 G; 114 T; 21 other;

RESULT 7

ABQ55585 standard; cDNA; 697

ABQ55585 ABQ55585 ID ABQ5 XX AC ABQ5 BP.

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Alphal(XVIII) collagen; mimetic; endostatin; atomic coordinate; library; anti-andiogenic; heparin binding domain; receptor binding domain; mimic; alpha-helix A domain; carbohydrate recognition domain; CRD domain; treatment; angiogenesis; tumour; human; ss.
                                                                                                                                                                                                                /product= "alphal(XVIII) collagen"
/note= "Partial sequence, no start codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying mimetics of mammalian endostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 5A-C, 75pp, English.
                                                                                                                                                                                 Location/Qualifiers
                                                                       Human alphal (XVIII) collagen cDNA.
 AAX78379 standard; cDNA; 3394
                                                                                                                                                                                                                                                                                                                             97US-0069727.
                                                                                                                                                                                                                                                                                                       98WO-US26783
                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Olsen BR,
                                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-395243/33.
                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY25113
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                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                      WO9931616-A1.
                                                                                                                                                                                                                                                                                                                             16-DEC-1997;
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                                                25-AUG-1999
                                                                                                                                                                                                                                                                             24-JUN-1999
                         AAX78379
                                                                                                                                                                                 Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A cDNA clone (AAT84484) codes for a human novel type alpha-1 (XVIII) collagen (AAW26327) that is expressed in multiple tissues, especially liver, lung and kidney. It was isolated from a placental cDNA library using a probe based on an unidentified collagenous protein and a probe based on mouse alpha-1 cDNA clone mc19. A claimed plasmid comprising alpha-1 collagen nucleic acid and an expression control sequence can be used to express recombinant collagen in prokaryotic or eukaryotic (especially mammalian) host cells. The collagen may be used to treat a patient suffering from a disease associated with degradation of cartilage, and for supplementing
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage
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                                                                                                                                                                                                                               Alpha-1 collagen; type XVIII collagen; cartilage degeneration;
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100.0%; Pred. No. 3.4e-06;
tive 0; Mismatches 0; Indels 0
 Length 697;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 3394 BP; 668 A; 1130 C; 1080 G; 516 T; 0 other;
4.2%; Score 35; DB 24;
100.0%; Pred. No. 3.8e-06;
ive 0; Mismatches 0;
                                                795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829
                                                                       282 ATGTAATCCTCAAGAATAAAAGGAAGCCAAAGAG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Column 23-30; 35pp; English
                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                   AAT84484 standard; cDNA; 3394 BP
                                                                                                                                                                                                       Human alpha-1 collagen cDNA.
                                                                                                                                                                                                                                                                                                                                                                             93US-0159784
                                                                                                                                                                                 (first entry)
 Query Match 4.2
Best Local Similarity 100.
Matches 35; Conservative
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P-PSDB; AAW26327.
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                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1993;
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                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degeneration
                                                                                                                                                                                 19-NOV-1997
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                                                                                                                                                          AAT84484;
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Best Local S
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Timpl R;

Sasaki T,

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mammalian endostation. The method comprises identifying unmerlies or mammalian endostation. The method comprises identifying unmerlies or having atomic coordinates with non-trivial similarity to selected coordinates of a mammalian endostatin involves (a) providing a library of atomic coordinates of compounds in a library of candidate compounds in a library of candidate compounds in a library of candidate compounds on the basis of selecting from the library at least one candidate compound on the basis of selecting from the library at least one candidate compound on the basis of selecting from the criteria which include similarities between the atomic coordinates of the mammalian criteria which include similarities between the atomic coordinates of the endostatin. The invention also describes the use of an anti-angiogenic fragment of endostatin comprising a domain selected from a heparin comprising and main exposed on alpha-helix A domain, and a carbohydrate recognition domain (CRD) domain. The methods can be used for treating endostatin minits. The compounds identified can be used for treating undesired anglogenesis, e.g. tumours. This sequence encodes human alphal(XVIII) collagen which is used in the description of the method.
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This invention describes a novel method for identifying mimetics of
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3.4e-06;
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100.0%; Pred. No. ...
... 0; Mismatches
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Best Local Similarity 100.
Matches 35; Conservative
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ABN95680
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ABN95680 standard; DNA; 3394 BP

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Gaps

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2187

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RESULT 9 AAX78379

795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829

35; Conservative

Matches

Similarity

Location/Qualifiers

Mus musculus.

Key

1..3867 /\*tag=

US5643783-A. 01-JUL-1997.

93US-0159784. 93US-0159784.

01-DEC-1993; 01-DEC-1993; HARD ) HARVARD COLLEGE

WPI; 1997-350247/32 Olsen BR;

oh SP,

P-PSDB; AAW26328

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                         Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                          Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3394;
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                                                                                                                                                                                                                                                                                                                      Vockley JG;
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100.0%; Pred. No. 3.4e-06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                 Gene #2178 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                      Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2178; 298pp; English.
                                                                                                                                                                                                                                   02-OCT-2001; 2001WO-US30589.
                                                                                                                                                                                                                                                               02-OCT-2000; 2000US-237054P.
                                       (first entry)
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                                                                                                                                                                                                                                                                                         (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                      Horne D, Alvares C,
                                                                                                                                                                                                                                                                                                                                                                                                                       liver tissue sample
                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-426119/45
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les 35; Conserv
                                                                                                                                                                             WO200229103-A2
                                                                                                                                                   Homo sapiens
                                       13-AUG-2002
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             ABN95680;
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A cDNA clone (AAT84485) codes for a mouse novel type alpha-1 (XVIII) collagen (AAW26328) that is expressed in multiple organs, especially the liver, lung and kidney. It was isolated by screening murine 15.5- and 17.5-day embryo libraries with probes based on murine type XII collagen and on human alpha-1 collagen cDNA. Isolated nucleic acids can be used to express recombinant alpha-1 collagen in transformed host cells. Claimed nucleic acid (see AAT84484) coding for human alpha-1 collagen (AAW26327) can be used to treat patients suffering from diseases associated with degradation of cartilage, and for supplementing collagen.

Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage

Disclosure; Fig 2; 35pp; English.

degeneration

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                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; generotestinal disorder; urinary system disorder; drug screening; generothestinal disorder; infection; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antinflammatory; gynaecological; reproductive; chromosome 21q22.3;
                                                                                Gaps
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0
                                     Length 4031;
                                                                                Indels
Seguence 4031 BP; 873 A; 1172 C; 1266 G; 720 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian antigen HEEBK29 cDNA, SEQ ID NO:835
                                                                                                                                                              3987 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 4021
                                     4.2%; Score 35; DB 18; L
100.0%; Pred. No. 3.4e-06;
tive 0; Mismatches 0;
                                                                                                                            795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829
                                                                                                                                                                                                                                                                               ABQ54955 standard; cDNA; 4875
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                                                            Best Local Similarity 100.
Matches 35; Conservative
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                                          Query Match
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ABQ54955
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Alpha-1 collagen; type XVIII collagen; cartilage degeneration; ss.

Mouse alpha-1 collagen cDNA.

(first entry)

19-NOV-1997

AAT84485

2187 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 2221

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AAT84485 standard; cDNA; 4031 BP

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nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiostatin, human or murine endostatin and angiogenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of phthalmological activity. The vector is used in gene therapy for expresses an anti-angiogenic, cytostatic, anti-diabetic and inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient.
                               Plasminogen; human; angiostatin; endostatin; gene therapy; collagen 18; anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina; vector; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel viral gene therapy vector comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5408 BP; 986 A; 1820 C; 1796 G; 806 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 75-76, 83pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bachelot T, Leboulch P, Pawliuk RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-angiogenic gene therapy vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-) GENETIX PHARM INC. (MASI ) MASSACHUSETTS INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI: 1999-357696/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1997;
                                                                                                                                                                                                                                                                   WO9926480-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to CDNAs encoding them (ABD54131-ABQ56305), and also encompasses polypeptides 99% identical and polybucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polymucleotides, antibodies against human ovarian antigens, and the use of ovarian antigens prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or preventing varian cancer, and breast cancer, and metastatic tumours of ovarian or sorgin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polyoystic ovary syndrome, ovarian cysts, and dysmenorinees), endocrine disorders, infections (e.g., chlamandyla, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders cand urinary system disorders. Ovarian antigen polypoptides and polynucleotides may also be used in screening for compounds which the ovarian antigen polypoptides may proceed the process of the polynucleotides may also be used in screening for polynucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the obtypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 4.2%; Score 35; DB 24; Length 4875; Best Local Similarity 100.0%; Pred. No. 3.4e-06; Matches 35; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 835; 2922pp; English.
                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                       07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                                                               07-JUN-2000; 2000US-209467P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA;
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WO200200677-A1
                                                                           03-JAN-2002
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TECHNOLOGY.

98WO-US24950. 97US-0975424.

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                              Gaps
                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38593.
                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                              .;
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                              Indels
    DB 20; Ld
3.3e-06;
hes 0;
                                                                              4202 ATGTAATCCTCAAGAATAAAAGGAAGCCAAAGAG 4236
                                                        795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829
     4.2%; Score 35; DB 100.0%; Pred. No. 3.3.3:ive 0; Mismatches
                                                                                                                                               AAK83781 standard; DNA; 37664 BP.
                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01354.
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Ouery Match
Best Local Similarity 100.0
Marches 35; Conservative
                                                                                                                                                                                                  07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                  WO200157182-A2.
                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                       RESULT 14
                                                                                                                                   AAK83781/
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0; Gaps

ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 3229 795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829

3195

ò g AAX77720 standard; DNA; 5408 BP

RESULT 13

Human collagen 18 DNA

10-AUG-1999

AAX77720;

EXHXHXB

Length 5408;

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2000US-0189874
2000US-0199874
2000US-0199123
2000US-020515
2000US-0209467
2000US-0215135
2000US-0215135
2000US-0215135
2000US-0216880
2000US-0216880
2000US-0216880
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2000US-0226681
2000US-0227182
2000US-0227182
2000US-0227009
2000US-0229287
2000US-0229344
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2000US-0229509
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2000US-0224519.
2000US-0225213.
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2000US-0225267.
2000US-0225268.
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2000US-0231244.
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2000US-0231414.
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2000US-0232081.
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2000US-0232397.
2000US-0232398.
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2000US-0232401.
2000US-0233063.
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2000US-0233065.
2000US-0234223.
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2000US-0234997.
2000US-0234998.
2000US-0235484.
     2000US-0180628
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2000US-0235836
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04-FEB-2000; 24-FEB-2000; 26-FEB-2000; 26-FEB-2000; 216-MAR-2000; 217-MAR-2000; 219-MAY-2000; 28-JUN-2000; 207-JUN-2000; 207-JUN-2000; 207-JUN-2000; 211-JUN-2000; 26-JUN-2000; 214-AUG-2000; 214-
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14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
18-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
23-AUG-2000; 2
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23-AUG-2000; 2
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25-SEP-2000;
27-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
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14-AUG-2000;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

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2000US-0229343.
2000US-0229344.
2000US-0229345.
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2000US-0241221.
2000US-0241785.
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2000US-0237037.
2000US-0237038.
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000US-0236369
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13-0CT-2000;
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06-SEP-2000;
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  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-deived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK64942 to AAK67950 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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Disclosure; SEQ ID NO 38593; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37664 BP; 6667 A; 11245 C; 10958 G; 8794 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.2%; Score 35; DB 22; Length 37664;
100.0%; Pred. No. 3e-06;
iive 0; Mismatches 0; Indels 0
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24-FEB-2000; 2000US-0180628.
26-MAR-2000; 2000US-0180550.
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19-MAY-2000; 2000US-025515.
07-JUN-2000; 2000US-025515.
07-JUN-2000; 2000US-0214886.
07-JUN-2000; 2000US-0214886.
07-JUL-2000; 2000US-021535.
07-JUL-2000; 2000US-0215135.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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Best Local Similarity 100.
Matches 35, Conservative
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Barash SC, Rosen CA,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 38594; 3071pp + Sequence Listing; English.

ARK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
cxpression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own produce the secreted (1), by inserting
polynucleotides may be used to produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.

Gaps Sequence 61710 BP; 11560 A; 18542 C; 18148 G; 13460 T; 0 other; ö Length 61710; Indels Query Match 4.2%; Score 35; DB 22; Le Best Local Similarity 100.0%; Pred. No. 2.9e-06; Matches 35; Conservative 0; Mismatches 0; S

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29908 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 29874 795 ATGTAATCCTCAAGAAATAAAAGGAAGCCAAAGAG 829 셤 ò

Search completed: August 17, 2003, 16:43:15 Job time : 321.86 secs

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1, Appli 5196516

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Perfect score:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08159784
Patent No. 5643783
GENERAL INFORTION:
CENERAL INFORTION:
CENERAL INFORTION:
CENERAL INFORTION:
CONTRESPONDENCE:
CORRESPONDENCE:
ADDRESSER:
Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 496.8; DB 1;
Pred. No. 5.3e-85;
0; Mismatches 157;
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US-08-458-568A-11
US-09-238-010-1
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US-09-231-818-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 1BM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
CLASSIFTCATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00246/170001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPA: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                  5196516-7
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Best Local Similarity 77.1%;
Matches 660; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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LENGTH: 3394
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Sequence 6920, Ap
Sequence 1, Apply
Sequence 1, Apply
Sequence 1793, Ap
Sequence 1793, Ap
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7, Appli
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4332.442 Million cell updates/sec
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Sequence 1, App
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                                                                                                                                           August 17, 2003, 13:57:19 ; Search time 84.4574 Seconds
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Sequence 12
Sequence 37
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Sequence 3,
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Sequence 1
Sequence 1
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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S-09-252-991A-12065
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-08-458-568A-11
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829
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us-09-938-391-1.rni

COMPUTER READABLE FORM:  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX COPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: Wordberfect (Version 5.1) CURRAY APPLICATION DATA: APPLICATION NUMBER: US/08/159,784 FILING DATE: December 1, 1993 CLASSIFICATION DATA: PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA:	FILING DATE:  ATTORNEY/AGENT INFORMATION:  NAME: John F. Freeman  REGISTRATION NUMBER: 29,066  REFERENCE/DOCKET NUMBER: 00246/170001  ; TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION 542-5070  TELEFAX: (617) 542-8906	; TELEX: 200154 ; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE TRARACTERISTICS: ; LENGTH: 4031 ; TYPE: nucleic acid ; TYPE: nicleic acid ; TOPOLOGY: single ; TOPOLOGY: 1inear	Query Match 51.0%; Score 423; DB 1; Le Best Local Similarity 76.9%; Pred. No. 3.5e-71; Matches 548; Conservative 0; Mismatches 150;	Qy 1 CCCTGGCGGCAGATGACATCCTGGCCGGCCCCCGGGCCT	3244	OY 118 GGGCCCGTCCACACCCACACCCACACCACAGACTTCCA	Qy 178 GCCCTGAACAGCCCGCAGCCGGGCGGCATGCGAGCATCCG	Oy 238 TTCCAGCAGGCGCGCGCGGGGGCTGGCCGGCACCTTCGG	Qy 298 CTGCAGGACCTCTACAGCATCGTGCGCGCGCGCCACCGCACGCA	Oy 358 CTCAGGACGAGGAGTGCTCTTCCCCAGCTGGGAGGCCTTATT	Oy 418 CTGAAGCCCGGGCCCCCATCTTCTCTTTCGACGCAGAGA	Qy 478 TGGCCCGGAAGAGCGTGGGCACGGCTCCGACCGGGG 1	Qy 538 TACTGCGAGACGTGGCGGACGGAGGCCCCGGCGGCCACCGG	Qy 598 GCGGGCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCCA
61 CCCGGGGCCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGTGGG	1546   CTCAACAGCCCCCTGTCAGGCGGCATGCGGGGGCCCGGGGGCCGACTTCCAGTGCTTC	Db   1666 CAGGACCTGTACAGCATGGCGCGCGCGCAGCGGCGCGCCATCGTCAACCTC 1725   Oy   361 AGGACGAGCTTTTCCCCAGGGCGAGCCTTTTCTCGGGCTCCGAGGCCAGCTG 420	1786 AAGCCCGGGCACGCATCTTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCCCCC	1848   CUCCAGAGAGCIGIGGCATGGCTCGACCCCAGGCGCAGGCTGACCAGAGCTAC 1905	Qy 601 GGCAGGCTGCTGGAGCAGGAGCCGCGAGCCGCCACGCCTTCGTGGTGCTCTGCATC 660	Qy         661 GAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGCCGGCC	721 GAGGGGCGCCGCAGGAGCATCCGCCCCGGGGG	757GGGCCTGGCCGGACGCTTGCCTGCACCG-TCACGTTTAATGTAATCCTCAAGAATA  1.1.1.	814 AAAGGAAGCCAAAGAG 829	SULT 2	US-0W-1597/84-1 US-Quence 1, Application US/08159784 ; Patent No. 5643783 ; GENERAL INFORMATION:	AFFLICANT: BJOTH K. OISEN TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:	ADDRES STREET CITY: STATE:	; COUNTRY: U.S.A. ; ZIP: 02110-2804

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ACCGGGGTGCCCGTCGAAC 357
                                                           CAGCCGGCTCGCCCCACTGGT 117
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                                                                                                                                                                                                                                                                                                                 GGGCAGGCGTCGCTGCTG 597
                            CTGCTGGACCCCCAGCCCTAC 60
                                                                                         CAGCTGGTGCTGCACCTGGTG 177
                                                                                                                        CGGGGACCGACTTCCAGTGC 237
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Length 4031;
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                                                                                                                           Sequence 4, Application US/09315689
Parent No. 6346510
GENERAL INFORMATION:
APPLICANT: FOLKman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
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Pred. No. 2.8e-70;
0; Mismatches 80;
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Best Local Similarity 85.3%;
Matches 466; Conservative
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SOFTWARE: PatentIn Ver. 2.0
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Patent No. 6346510
GRNERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: OF TREILLY, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
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Pred. No. 2.8e-70;
0; Mismatches 80;
Sequence 30, Application US/09206059
Patent No. 6201104
GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas
APPLICANT: Sim, Kim Lee
TITLE OF INVENTION: Andiogenesis-Inhibiting Pro;
TITLE OF INVENTION: Andiogenesis-Inhibiting Pro;
TITLE OF INVENTION: Procesins and Methods of Use
FILE REFERENCE: 05213-0370
CURRENT APPLICATION NUMBER: US/09/206,059
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.3%;
Matches 466; Conservative
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; ORGANISM: Homo sapiens
US-09-206-059-30
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APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVANTION: ANTIBOY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/561,108
CURRENT FILING DATE: 2000-04-28
PRIOR PRILICATION NUMBER: 60/131,432
PRIOR PRILICATION DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 573
                                                                                                                                                                                                                                          126 CCACACCCACACCCACCCACCAGGACTTCCAGCTGCTGCTGCTGCTGGTGGCCCTGAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 CGAGGTGCTAICTCCCAGCTGGGACTCCCTGTTTTCTGGCTCCCAGGGTCAACTGCAACC 308
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
LOCATION: (1)..(573)
                                                                                                                Score 376.8; DB 4;
Pred. No. 1.4e-62;
0; Mismatches 117;
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                                                                                                                Query Match
Best Local Similarity 79.3%;
Matches 447; Conservative
                         ; LOCATION: (1)..(573)
US-09-561-500-12
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-09-561-108-12
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Fatent No. 6342219

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF

CURRENT APPLICATION NUMBER: US/09/561,500

CURRENT FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR PLILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 12

SEQ ID NO 12

LENGTH: 573
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                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                           Score 410.8; DB 4;
Pred. No. 6.2e-69;
0; Mismatches 77;
CURRENT APPLICATION NUMBER: US/09/315,689
                         CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.6%;
Matches 457; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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US-09-561-500-12
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Length Indels

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Score 376.8; DB 4;
Pred. No. 1.4e-62;
0; Mismatches 117;
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45.5%;
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ORGANISM: Artificial Sequence
FEATURE:
                  Best Local Similarity 79.3
Matches 447; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (1)..(573)
US-09-561-499-12
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APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Solf A. Brekken
TILE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002586
CURRENT APPLICATION NUMBER: US/09/561,526
CURRENT FILING DATE: 2000-04-28
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                                                                                                  126 CCACACCCACACCCACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGCCCCTGAA
                                                                      Gaps
                                                                     .;
0
                                  DB 4; Length 573;
                                Score 376.8; DB 4; Length
Pred. No. 1.4e-62;
0; Mismatches 117; Indels
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; Patent No. 6416758
                                  45.5%;
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                              Query Match
Best Local Similarity 79.3
Matches 447; Conservative
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PRIOR FILING DATE: 1999-0
NUMBER OF SEQ ID NOS: 44
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; LOCATION: (1)..(573)
US-09-561-526-12
JS-09-561-108-12
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SEQ ID NO 12
LENGTH: 573
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Patent No. 6524583
GENERAL INFORMATION
FAPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002582
CURRENT APPLICATION NUMBER: 08/09/561,499
CURRENT PILING DATE: 2000-04-28
PRIOR PRIOR TO NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 573
                                                                                                                                                                   69 CACCCCCTGTCTGGAGGCATGCGTGGTATCCGTGGAGCAGATTCCAGTGCTTCCAGCA
126 CCACACCCACACCCACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCCCCTGAA
                                        9 CCATCACCATCACCATACTCACAGACTTTCAGCCAGTGCTCCACCTGGTGGCACTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 376.8; DB 4;
Pred. No. 1.4e-62;
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Patent No. 6267954
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693
NAME: MCMOSTOW Jr., Robert TELECOMUNICATION INFORMATION: TELEPHONE: (302) 658-5613 INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
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                                                                                                   LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 445; Conservative
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                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                    US-08-985-526-37
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Mixson, James A
APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Connolly, Bove, Lodge, & Hutz
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                                                                                                                            CACCCCCTGTCTGGAGGCATGCGTGTATCCGTGGAGCAGATTTCCAGTGCTTCCAGCA 128
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                                                        CCATCACCATCACCATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTGGCACTGAA
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Mismatches 117; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
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ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Delaware
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-985-526-37
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126 186 366 135 CACCCACACCACCAGGACTTCCAGCTGGTGCTGCACCTGGAGCGCCCTGAACAGCCCGCA 194 254 314 374 246 434 306 494 554 426 614 486 674 546 99 127 CGTGGGGCTGTCGGGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAG 67 Grendgaggeargegranecargagacagarirecagrecriceaggaageeegage CGCGGGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAG 187 CATCGTGCGCCGTGCTGACCGGGGTCTGTGCCCCATCGTCAACCTGAAGGACGAGGTGCT 247 ATCTCCCAGCTGGGACTCCCTGTTTTCTGGCTCCCAGGGTCAACTGCAACCCGGGGCCCG 307 CATCTTTCTTTGACGCAGAGATGTCCTGAGACACCCAGCCTGGCCGCAGAGAGGGGT 495 GTGGCACGGCTCCGACCCCAGCGGGCCCCTGACCGACAGCTACTGCGAGACGTGGCG 555 GACGGAGGCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGCTGGCGGGCCAGGCTGCTGGA 7 cargearacrearcadeactrreagecagrecrecaceregregeacreaaceceer 375 CTTCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCCAGCTGAAGCCCGGGGCCCG 615 GCAGGAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCAT CATCTTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCCGGAAGAGCGT CATCGTGCGCCGCCGGACCGCACCGGGGTGCCCGTCGACCTCAGGGACGAGGTGCT Gaps APPLICANT: Ureza, Yves
APPLICANT: Wensache, Maurice
APPLICANT: Bossard, Carine
APPLICANT: Bossard, Carine
APPLICANT: Sonnel, Sebastien
APPLICANT: Bonnel, Sebastien
APPLICANT: Honiger, Jiri
APPLICANT: Honiger, Jiri
APPLICANT: Honiger, Jiri
APPLICANT: Meuner-Jehle, Martin
TITLE OF INVENTION: INTRACOCTILAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.2020S01 ; 0 565; Length

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Sequence 6774, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6774
LENGTH: 741
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Pred. No. 1.9e-62;
0; Mismatches 113;
          PRIOR APPLICATION NUMBER: US 09/449,293
                                PRIOR FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 558

TYPE: DNA

ORGANISM: Rattus rattus
US-09-775-325-3
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Best Local Similarity 79.7%;
Matches 444; Conservative
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US-09-252-991A-6774
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APPLICANT: Menasche, Maurice
APPLICANT: Menasche, Maurice
APPLICANT: Bossard, Carine
APPLICANT: Bonnel, Sebastian
APPLICANT: Bonnel, Sebastian
APPLICANT: Herve
APPLICANT: Herve
APPLICANT: Herve
APPLICANT: Neuner-Jehle, Martin
TITLE OF INVERTON: INTRACCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.2020501
CURRENT APPLICATION NUMBER: US/09/775,325
CURRENT FILING DATE: 2001-02-01
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                                                                                                                                                                                                                                                                                                                                                       Score 376.2; DB 3; Length
Pred. No. 1.9e-62;
0; Mismatches 113; Indels
CURRENT APPLICATION NUMBER: US/09/449,293
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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Patent No. 650049
GENERAL INFORMATION:
APPLICANT: Abitbol, Marc
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Best Local Similarity 79.7%;
Matches 444; Conservative
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                                                                                                                                                                                   LENGTH: 558
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US-09-775-325-3
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919

257

317

377 434 374

557

734 137 674 197 614

us-09-938-391-1.rni

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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                0; Mismatches 359;
                                                                        Score 65.6; DB 4;
Pred. No. 0.00027;
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PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-19
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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SEQ ID NO 6824
LENGTH: 1590
                                                                                                                                                Matches 281; Conservative
                                                                                                          Similarity
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   US-09-252-991A-6920
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                                                                            Query Match
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Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NO 6920
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                                                                                                                                                                                                                                                                                                                                                                 64 CATICICGGICCCTGCGCCTTCCCGCCGGAGCCGGTGACCAACGTCCTCGGCGAGTACCT 123
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Pred. No. 0.00027;
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6774
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US-09-252-991A-6920/c
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Query Match 7.9%; Score 65.6; DB 4; Length 1590; Best Local Similarity 43.9%; Pred. No. 0.00027; Matches 281; Conservative 0; Mismatches 359; Indels 0
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		34, Appl	50, Appl	2178, Ap	144, App	, Appli	3, Appli	53, Appl	), Appl	2, Appli	51, Appl	5, Appli	59, Appl	18, Appl	12, Appl	37, Appl	
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SUMMARIES	ID	US-10-292-418-34	US-10-131-241-50	US-09-880-107-2178	US-10-060-036-144	US-10-042-347-4	US-10-292-418-3	US-10-131-241-53	US-09-873-676-30	US-10-080-797-2	US-10-131-241-51	US-10-042-347-6	US-10-131-241-59	US-10-131-241-48	US-09-998-831-12	US-10-036-869-37	C 177 - 377 - 90 - 911
	 DB	12	14	10	14	14	12	14	0	13	14	14	14	14	10	13	0
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	* Query Match	66.4	66.4	59.9	59.5	50.4	50.4	50.4	50.4	50.3	50.1	49.6	49.6	48.6	45.5	45.4	u
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3, Appl 14, App 115, Ap 1159, Ap 1159, Ap 115103, 115103, 115103, 115103, 115103, 115103, 115103, 115103, 115103, 113, Appl 113, Appl 119, Appl 11	Sequence 6094, Ap Sequence 4052, Ap Sequence 1, Appli Sequence 1, Appli
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                                                                                                                                                                                                                                                   ; LOCATION: (1)..(552)
; OTHER INFORMATION: Endostatin
US-10-292-418-34
                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
                                                                                                                                                                                                                                          NAME/KEY: CDS
RESULT 1
US-10-292-418-34
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259 GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGGGGCTGCAGGACCTCTACAGCATC	Db 181 GTGCGCGGCGGCGGCGGGGGGGGGGGGGGGGGGGGGGG	301 TTCTCTTTCGACGACGAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGG 499 CACGGCTCCGACCCCAGCGCGCCGCCTGACCGACACGCAACAGCTGCGACC 640 CACGGCTCCGACCCCAGCGCGCCGCCTGACCGACGCTACTGCGAACGTGGCGGACGCGACGTGCTGCACCGACGTGCTGCGACGTGCGGACGTGCTGCACCGACGTGCTGCACCGACGTGCTGCACCGACGTGCTGCACGTGCTGCACGTGCTGCACGTGCTGCACGTGCTGCACGTGCTGCACGTGCTGCACGTGCTGCACGTGCTGCACGTGCTGCACGTGCACGTGCTGCACGTGCACGTGCACGTGCACGTACACACGTACACACGTACACACGTACACACAC	Db 361 CACGGCTCCGACCCCAGCGGCGCCCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420 Oy 559 GAGGCCCCGGCGCCACCCGGGCAGCGTCGCTGCTGCTGCGAGCAGCTGCTGCTGGAGCAG	4.21 GAGGCCGCGGCGCCGCCGCCGCGCGCGCGCGGGGGGGGG	Db 481 GAĞGCGGGĞAĞCTĞCGCCĞCĞCĞTÇĞTĞĞTĞĞATÇĞAĞAAÇAĞCGTÇATĞAĞÇ 540 Qy 679 TÇTTÇTÇÇAĞ 690	Db 541 TCTTCTCAAG 552	11 trion US/0 12 trion US/0 12 trion US/0 13 trion US/0 14 trion US/0 15 trion US/0 16 trion US/0 17 trion US/0 18 trion US/0 18 trion US/0 19 trion US/0 19 trion US/0 10 tri	Best Local Similarity 77.1%; Pred. No. 8.1e-108; Best Local Similarity 77.1%; Pred. No. 8.1e-108; Matches 660; Conservative 0; Mismatches 157; Indels 39; Gaps	1 CCCTGGCGGCAGATGACATCCTGGCCGGCCCCCCCGCTGCTGGACCCCCAGCCCTAC  1378 CCCTGGCGGCAGATGACATCCTGGCCAGCCCCCTGGGCTGCCGAGCCCTAC	0y 61 CCCGGGGCCCGCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCTGGTGGG 120
61 GGCGCATGCGAGGCATCCGGGAGCGGACTTCCAGTGCTTCCAGCAGGCGCGCGC	0y         319 GTGGCGCGGCGGCGACCGGGGGGGCGCGTCAACGGACGAGGGTGCTTC         378           1	439 TTCTCTTTCGACGCAGAANGTCCTGCAGCCCCCCCCTGGCCCCGGAAGACGTGTGGCCCCGGAAGAGCGTGTGGCCCCGCCTGCCCCCGGAAGAGCGTGTGGCTCTGCAGCCCCCGCCCTGGCCCCCGGCCCCGGAAGAGCGTGTGGCCCCGGCCCCGGAAGAGCGTGTGGCCCCGGCCCCGGAAGAGCGTGTGGCCCCGGCAAGAGCGTGTGGC	499 CACGCTCCGACCCCAGCGGCGCCCCTGACCGACACCTGCGACACGTGGCGGACG		Qy         619         GAGGCCGCAGGCCCCCCCCCCCCTCGTGGTGCTCTCCAGAACAGCGTCATGACC         678	Oy 679 TCCTTCTCCAAG 690 Db 541 TCCTTCTCCAAG 552	RESULT 2 US-10-131-241-50 is Sequence 50, Application US/10131241 is Publication No. US20030012792A1 is Publication No. US20030012792A1 is Publication No. US20030012792A1 is Publication No. US20030012792A1 is APPLICANT: Holaday, John W. APPLICANT: Holaday, John W. APPLICANT: Holaday, John W. APPLICANT: Fortier, Anne H. TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer TITLE OF INVENTION: UNMBER: US 130-271565 CURRENT APPLICATION NUMBER: US 09/413,049 PRIOR APPLICATION NUMBER: US 09/413,049 PRIOR FILING DATE: 1999-10-06 PRIOR PAPLICATION NUMBER: US 60/086,586 PRIOR FILING DATE: 1999-05-22 NUMBER OF SEQ ID NOS: 65 SOFTWARE: PatentIn version 3.1 SEQ ID NO 50 LENGTH: 552 TYPE: DNA ORGANISM: Canine sp. US-10-131-241-50	Query Match Best Local Similarity 99.8%; Pred. No. 2.2e-120; Matches 551; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy         139 CACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGACGAGCCGCAGCCG         198           Db         1 CACACCCACCAGGACTTCCAGCCGGTGCTGCTGGTGGCCCTGAACAGCCGCAGCCG         60	Oy 199 GGCGGCATGCGAGGCATCCGGGGAGCGGCTTCCAGTGCTTCCAGCAGCGCGCGC

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661 GAGAACAGCGTCATGACCTCCTTC 684
; ORGANISM: Homo sapiens
US-10-060-036-144
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US-10-060-036-144

US-10-060-036-144

Sequence 144, Application US/10060036

Publication No. US20030073144A1

GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Appler, Michael D.
APPLICANT: Hepler, William T.
APPLICANT: Janay, Yuqiliam T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 21012.1 566
CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SEQ ID NO 144

LENGTH: 4551

TYDE: NAME ASSI
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Sequence 4, Application US/10042347
Sequence 4, Application US/10042347
Publication No. US20030114370A1
GENERAL INFORMATION:
APPLICANT: FOlkman, M. Judah
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: UNCLEAC Acid Molecules Encoding Endostatin Protein and Peptide Fri
TITLE OF INVENTION: Thereof
FILE REFERENCE: 05213-0880 (43170-249874)
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 09/315,689
PRIOR FILING DATE: 1998-10-30
PRIOR PELING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: US 09/154,302
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                                             12; Gaps
Length 4551,
                                             Indels
DB 14;
Query Match 59.5%; Score 493.2; DB 14; Best Local Similarity 83.9%; Pred. No. 5.6e-107; Matches 574; Conservative 0; Mismatches 98;
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Sequence 53, Application US/10131241
Publication No. US20030012792A1
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer:
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
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CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09383,315
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 3
LENGTH: 549
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LOCATION: (1)..(549)
OTHER INFORMATION: endostatin
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ORGANISM: Homo sapiens
FEATURE:
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US-10-131-241-53
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Publication No. US20030139365A1
GENERAL INFORMATION:
APPLICANT: Lo, Kin-Ming
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Anglogenesis Inhibitors
TITLE OF INVENTION: Immunofusins
FILE REFERENCE: LEX-006C1
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Pred. No. 2.9e-89;
0; Mismatches 80;
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: US 08/740,168
PRIOR FILING DATE: 1996-10-22
PRIOR FILING DATE: 1995-10-23
PRIOR FILING DATE: 1995-10-3
PRIOR APPLICATION NUMBER: US 60/023,070
PRIOR APPLICATION NUMBER: US 60/024,070
PRIOR APPLICATION NUMBER: US 60/026,263
PRIOR FILING DATE: 1996-09-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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Matches 466; Conservative
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Publication No. US20020183253A1
GENERAL INFORMATION:
APPLICANT: Campochiaro, Peter A.
APPLICANT: Dixon, Katharine H.
APPLICANT: Brazzell, Romlus K.
TITLE OF INVENTION: METHOD FOR TREATING OCULAR
TITLE OF INVENTION: METHOD FOR TREATINO
FILE REFERENCE: 4-31881A
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 418; DB 9;
Pred. No. 2.9e-89;
0; Mismatches 80
                                                       60/289,387
        PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 552
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.4%;
85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.4
Best Local Similarity 85.3
Matches 466; Conservative
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US-10-080-797-2
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Pred. No. 2.9e-89;
0; Mismatches 80;
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CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN VERSION 3.1
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Patent No. US20020077289A1
GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas J.
APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sch
al Similarity 85.3%;
466; Conservative
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Best Local Similarity
Matches 466; Conserv
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US-09-873-676-30
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Sequence 6, Application US/10042347

Sequence 6, Application US/10042347

Publication No. US20030114370A1

GENERAL INFORMATION:

JAPPLICANT: FOIkman, M. Judah

TITLE OF INVENTION: NUCLEIC Acid Molecules Encoding Endostatin Protein and Peptide Free

TITLE OF INVENTION: NUCLEIC Acid Molecules Encoding Endostatin Protein and Peptide Free

TITLE OF INVENTION: Thereof

FILE REFERENCE: 05213-0880 (41170-249874)

CURRENT FILING DATE: 1080-05-10

PRIOR APPLICATION NUMBER: US 60/106,343

PRIOR APPLICATION NUMBER: US 60/106,343

PRIOR FILING DATE: 1998-09-16

PRIOR APPLICATION NUMBER: US 60/106,383

PRIOR FILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-23
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                                                                             DB 14; Length 632;
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                                                                     Score 415.6; DB 1
Pred. No. 1.1e-88;
0; Mismatches 29
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                                                                         Query Match
Best Local Similarity 82.8%;
Matches 523; Conservative
US-10-131-241-51
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; Publication No. US20030012792A1
; Publication No. US20030012792A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL REPLICANT: Holaday, John W.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT APPLICATION NUMBER: US 90/413,049
PRIOR FILING DATE: 1999-10-06
; PRIOR FILING DATE: 1999-0-6-21
PRIOR PELING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-05-22
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                                                                                                                                                      Score 417; DB 13; Length 5
Pred. No. 5e-89;
0; Mismatches 80; Indels
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity
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ORGANISM: Murinae
; TYPE: DNA
; ORGANISM: Human
US-10-080-797-2
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APPLICANT: Holaday, John W.

APPLICANT: Holaday, John W.

APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

FILE REFERENCE: 05213-0344 43170-271565

CURRENT APPLICATION NUMBER: US 09/413,049

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR APPLICATION NUMBER: US 09/316,802

PRIOR APPLICATION NUMBER: US 09/316,802

PRIOR PRILING DATE: 1999-05-21

PRIOR PLILING DATE: 1998-05-21

PRIOR PLILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PARCHING PATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SEQ ID NO 48

LENGTH: 540
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                                                                                                                                   Length 537;
                                                                                                                                 Score 410.8; DB 14; Length
Pred. No. 1.4e-87;
0; Mismatches 77; Indels
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Sequence 48, Application US/10131241
Publication No. US2030012792A1
GENERAL INFORMATION:
                                                                                                                                   49.6%;
85.6%;
                                                                                                                             Query Match
Best Local Similarity 85.6°
Matches 457; Conservative
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US-10-131-241-48
                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-241-59
        SEQ ID NO 59
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Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

CURRENT PILLING DATE: 2002-07-22

PRIOR FILLING DATE: 1999-05-21

PRIOR FILLING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 09/316,802

PRIOR APPLICATION NUMBER: US 09/316,802

PRIOR PILLING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

NUMBER OF SEQ ID NOS: 65
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Pred. No. 1.4e-87;
0; Mismatches 77; Indels 0;
PRIOR APPLICATION NUMBER: US 60/023,070
PRIOR FILING DATE: 1996-08-02
PRIOR PPLICATION NUMBER: US 60/026,263
PRIOR FILING DATE: 1996-09-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
LENGTH: 534
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.6%;
Matches 457; Conservative
                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-10-042-347-6
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APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
TITLE OF INVENTION: INHIBITING VEGF
FILE REFERENCE: 4001.002564 831
CURRENT APPLICATION NUMBER: US/09/998,831
CURRENT FILING DATE: 2001-11-30
PRIOR PAPLICATION NUMBER: 09/561,108
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VOS: 42.0
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 Length 540;
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                             85; Indels
Score 403; DB 14;
Pred. No. 9.7e-86;
0; Mismatches 85;
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Query Match
Best Local Similarity 84.2%;
Matches 454; Conservative
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; LOCATION: (1)..(573)
US-09-998-831-12
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US-09-998-831-12
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LENGTH: 573
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Sequence 37, Application US/10036869
Publication No. US20020151516A1
GENERAL INFORMATION:
APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: THERAPY
THERAPY
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STRET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEPHONE: (302) 658-9141
SEQUENCE CHARACHERISTICS:

TYPE: nucleic acid
STRANDEDDESS: single
TOPOLOGY: linear

US-10-036-869-37
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BE9112588 602990468
CB44165 695295 MA
BU859398 AGENCOURT
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BM126109 602025454
BM1247582 602960041
BM123254 AGENCOURT
BM1613 601776586
BM1632049 UI -H-FE1-

Scoring table:

Searched:

Minimum DB Maximum DB

Database

score:

Title: Perfect

Sequence:

OM nucleic

Run on:

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Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM424 row: g column: 24
High quality sequence stop: 689.,
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NIH-MGC http://mgc.nci.nih.gov/.
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AGENCOURT 14021788 NIH MGC 179 Homo sapiens cDNA clone
IMAGE:30365831 5', mRNA sequence.
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BF166139
BU632049
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AW192502
BU352506
BG967333
AA288198
AI970297
AW243446
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BU859398
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BM683067
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AV696242
CB596713
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BF384828
CB424313
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AI326391
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VERSION
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DEFINITION
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AUTHORS
TITLE
JOURNAL
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CD105862
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 CD105862 AGENCOURT
BQ672290 AGENCOURT
BQ673186 AGENCOURT
BF074459 221883 MA
                                                                                                       August 17, 2003, 13:19:37; Search time 2416.32 Seconds (without alignments) 8338.472 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                             nucleic search, using sw model
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BQ672290
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                                                                                                                                                                                                                                         IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Result No.

A1858615 w140f01.x BU540812 AGENCOURT BI147444 602914008 BM9998137 UI-H-DTI-BQ772348 UI-H-EZI-AM92502 x145610.x BU352506 603527982 BG96733 602833649 AA288198 vb15b10.r A1970297 w109002.x AN243446 xm95d11.x BI219399 602936756

CB216999 NISC nq11 BU459935 603367327 BF384828 602046324 CB424313 598557 MA

EST 15-MAY-2003

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AGENCOURT 8354946 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275261
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                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2458 row: column: 06
High quality sequence stop: 588.
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                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                         BQ672290
BQ672290.1 GI:21783124
                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                            Homo sapiens (human)
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/clone="InfAGE:30365831"
/tissue_type="Pituitary"
/lab_host="Pituitary"
/lab_host="Pituitary"
/lab_host="Pituitary"
/clone_lib="NIH MGC 179"
/note="Corgan: Drain; Vector: pCWV-SPORT6.1; Site_1: EcoRV (destroyed); Site_2: Not1; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning)
. Average insert size 1.1 kb. Library was constructed by (Invitrogen) 278 g 124 t
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Pred. No. 7.7e-85;
0; Mismatches 98;
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Local Similarity 83.9%;
les 574; Conservative
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1 (bases 1 to 551)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749 GCATTGAGAACAGCTTCATGACTGCCCTC-CAAGAAACCACGCCTGGAATGCGGAATGG
                                                                                                                                                       CCTGGCGGCAGATGACATCCTGGCCAGCCCCCCCCTGGCCTGCCCGAGCCCAGCCCTAC
                                                                                                                                                                                                        CCCGGGGCCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGTGGG
                                                                                                                                                                                                                                                                                    CCCGTCCACACCCACCCACCCACCACCACCTTCCAGCTGCTGCTGCTGGTGGTGGTGGTGGTGCT
                                                                                                                                                                                                                                                                                                                            CTGAACAGCCCGCAGCCGGGCGGCATGCGAGGCATCCGGGGAAGCGGACTTCCAGTGCTTC
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                                                                                                                        CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCCCGGCCTGCTGGACCCCCAGCCCTAC
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                                          Length 979;
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                                        Score 451; DB 13; Length 9 Pred. No. 9.4e-77; 0; Mismatches 145; Indels
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BF074459.1 GI:10867970
                                          54.4%;
larity 78.8%;
Conservative
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                                                             Similarity
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/mol_type="mRNA"
/db_type="mRNA"
/db_type="mRNA"
/clone="IMAGE:627287"
/tissue_type="epidermoid carcinoma, cell line"
/tissue_type="epidermoid carcinoma, cell line"
/tissue_type="epidermoid carcinoma, cell line"
/tab_host="NHH OB (phage-resistant)"
/clone_lib="NHH MGC_102"
/note="Organ: salivary gland, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGGACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                979 bp mRNA linear EST 15-JUL-2002
8414390 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6272287
480
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                                                                                                                                                                    TGCGAGACGTGGCGGACGGAGGCCCCGGGCGACCGGGCAGGGGTCGTCGTCGCTGCTGGCG 600
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                                                                                      509 AAGCCCGGGGCACGCATCTTCTCCTTTAACGGCAAGGACGTCCTGAGGCACCCCACCTGG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATG

CDN Library Preparation: Rubin Laboratory

CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLCMA450 row: g column: 08

High quality sequence stop: 638.
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5', mRNA Sequence.
BQ673186
BQ673186.1 GI:21784020
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Mammalia, Eutheria,
1 (bases 1 to 979)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 GCGGACTTCCAGTGCTTCCAGCAGCGCGCGCGCGGGCTGGCCGGCACCTTCCGGGCC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 GTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTCCGAGGCCCAGCTGAAGCCCGGGGCCCGCATCTTCTCTTTCGACGCAGAGATGTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAGCACCCCGCCTGGCCCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCCAGCGGGGGG
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Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 GTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCGGGCGCGTGCGAGGCATCCGGGGA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATCGTGCGCCGCGCCGACCGCACCGGG 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGTCGTCGCTGCTGGCGGGCAGGCTGCTGGAGGCAGGAGGCCGCGAGGCTGCCGCCACGCC
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                                                                                                                                                                                                                                                                                     Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4336
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 445.2; DB 1
Pred. No. 1.2e-75;
0; Mismatches 63
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PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 81 row: F column: 9
Seq primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled"
/lab_host="DH108"
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88.5%;
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Best Local Similarity
                                                                                                       Keele, J.W.
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| Wall | Wall
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BG387051
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                                                     481 TTCATTGTCCTCTGCATCGAGAACAGCTTCATGACCTCCTCCTCCAAGTAGGGCCTCTGC 540
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643 TTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACCTCCTTCTCCAAGTAGGGCCGCGCG 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 832)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Sitatagene) and Superscript II RT (Life Technologies)" (7320 c 265 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
thtp://inage.llnl.gov
Plate: LichiloG row: a column: 14
High quality sequence stop: 679.
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Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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BP230015B10C11 Soares normalized bovine placenta Bos taurus CDNA
clone BP230015B10C11 5', mRNA sequence.
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1 (bases 1 to 279)

Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 ValAsnLeuArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGlu 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 GlyGlnLeuLysProGlyAlaArgIlePheSerPheAspGlyArgAspValLeuGlnHis 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="pooled"
/lab.host="DH10B"
/clome_lib="WARC 1PIG"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 GTTAACCTCAGGGACGAGGTGCTGTTCCCCAGCTGGGAGGCCTTGTTCTCGGGCTCTGAG
                                                                                                      USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4369 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
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Plate: 89 row: K column: 13
Seq primer: ATTTAGGTGACATATAG.
Location/Qualifiers
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Unpublished
Contact: Lewin, H. A.
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                                                                                     Contact: Smith TPL
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Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise-T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J. and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
                                                                                                                                                                                                                                         Figure 1. Smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
      Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keele,J.W.

Porcine gene discovery by normalized cDNA-library sequencing and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 GlyGlnLeuLysProGlyAlaArgIlePheSerPheAspGlyArgAspValLeuGlnHis 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GGCCAGCTGAAGCCCGGCGCCCCGCATCTTCTTTTCGACGGCAGAGACGTCCTTCAGCAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 GTTAACCTCAGGGACGAGGTGCTGTTCCCCAGCTGGGAGGCCTTGTTCTCGGGCTCTGAG 93
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/mol type="mRNA"
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Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4390
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BACKWARD: GTTTTCCCAGTCACGACG
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Db

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

; Search time 2038.89 Seconds (without alignments) 2741.704 Million cell updates/sec August 18, 2003, 00:28:06 Run on:

US-09-938-391-2 Title: Perfect score:

230 1 PWRADDILAGPPRLLDPQPY......CRHAFVVLCIENSVMTSFSK 230 Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0 OLIGO Scoring table: Sequence:

22781392 segs, 12152238056 residues Searched:

Word size:

45562604 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Database

EST:\*

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29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

EST 12-MAR-2001

BG383960 451 bp mRNA linear 302432 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence BG383960.1 GI:13308432 Sus scrofa (pig) Sus scrofa EST. ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION RESULT 1 BG383960

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus. 1 (bases 1 to 451)
Pahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., REFERENCE AUTHORS

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Sequence 17, Application US/10292418

Sequence 17, Application WS/10292418

Publication No. US20030139365A1

GENREAL INFORMATION:

APPLICANT: Lo, Kin-Ming

APPLICANT: Li, Yue

APPLICANT: Lo, Kin-Ming

FILE REFERENCE: Lex-006c1

CURRENT APPLICATION NUMBER: US/10/292,418

CURRENT FILING DATE: 2002-11-12

PRIOR FILING DATE: 1999-08-25

PRIOR FILING DATE: 1998-08-25

NUMBER: O SEQ ID NOS: 54

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 17

LENGTH: S52
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                                                                                                                                                                                                                                                                                            130 GGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATCGTGCGCCGT
                                                                                                                                                                                                                                                                        90 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArg
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GRANISH: Mus musculus
FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(552)

OTHER INFORMATION: endostatin
US-10-292-418-17
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is Sequence 48, Application US/10131241
is Publication No. US20030012792A1
is Publication No. US20030012792A1
is GENERAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Holaday, John W.
ITILE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
ITILE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
ITILE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
ITILE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
ITILE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
CURRENT APPLICATION NUMBER: US 09/413,049
is PRIOR FILING DATE: 1999-105-21
is PRIOR FILING DATE: 1999-05-21
is PRIOR FILING DATE: 1999-05-22
is NUMBER OF SEQ ID NOS: 65
is SOFTWARE: PatentIn Version 3.1
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                      1624 GGGCTGGCGGCACCTTCCGCGCCTTCCTGTCGCGCCTGCAGGACCTGTAGAGCATC 1683
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87 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                   Sequence 144, Application US/10060036
Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodge, Michael D.
APPLICANT: Decising, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT PILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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26.00
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Query Match:
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US-10-060-036-144
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LENGTH: 4551
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LENGTH: 540
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Query Match:

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Pred. No.: Score:

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455 GGGCTGGCGGCCATCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 514
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L22548
US-09-880-107-2178
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APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Generf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR PELLING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2178
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 21012.1.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
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Patent No. US20020142981A1
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ORGANISM: Homo sapiens
US-10-060-036-64
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APPLICANT: Sim, Kim L.
APPLICANT: Sim, Kim L.
TILE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use FILE REPERENCE: 05213-0378 (43170-25933)
CURRENT APPLICATION NUMBER: US/09/873,676
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 60/209,065
PRIOR APPLICATION NUMBER: US 60/209,387
PRIOR PILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.1
ENGTH: 552
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Matches:
        NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-10-080-797-2
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US-10-060-036-64
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Pred. No.:
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APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION: Immunofusins
FILE REFERENCE: LEX-006C1
CURRENT APLICATION NUMBER: US/10/292,418
FRIOR APPLICATION NUMBER: US/33,315
FRIOR APPLICATION NUMBER: US/33,315
FRIOR FILING DATE: 1999-08-25
FRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
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Matches:
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CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION WUMBER: US 09/315,689
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: US 09/154,302
PRIOR APPLICATION NUMBER: US 08/740,168
PRIOR PILING DATE: 1998-10-22
PRIOR FILING DATE: 1996-10-22
PRIOR FILING DATE: 1996-10-23
PRIOR FILING DATE: 1996-10-23
PRIOR PLICATION NUMBER: US 60/023,070
PRIOR PLICATION NUMBER: US 60/023,070
PRIOR PLING DATE: 1996-09-17
PRIOR PLING DATE: 1996-09-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10292418; Publication No. US20030139365A1; GENERAL INFORMATION:
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OTHER INFORMATION: endostatin
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
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LENGTH: 546
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LENGTH: 549
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US-10-292-418-3
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Sequence 53, Application US/10131241

Sequence 53, Application US/2030012792A1

Publication No. US20030012792A1

GENERAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifers
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-105-21

PRIOR PLING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 60/086,586

PRIOR APPLICATION NUMBER: US 60/086,586

PRIOR PILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.1

LENGTH. 549
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Fublication No. US20020183253A1
Fublication No. US20020183253A1
FUBLICANT: Campochiaro, Peter A.
APPLICANT: Dixon, Katharine H.
APPLICANT: Brazzell, Romulus K.
TITLE OF INVENTION: METHOD FOR TREATING OCULAR
TITLE OF INVENTION: NEOVASCULARIZATION
FILE REPERENCE: 4.31881A
CURRENT APPLICATION NUMBER: US/10/080,797
CURRENT FILING DATE: 2002-02-21
  Matches:
Conservative:
                                               Mismatches:
Indels:
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WS-10-131-241-59

Sequence 59, Application US/10131241

PUBLICANT: Holaday, John W.

APPLICANT: Holaday, John W.

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT FILING DATE: 1999-10-06

PRIOR PALING DATE: 1999-10-06

PRIOR PAPLICATION NUMBER: US 09/316,802

PRIOR PAPLICATION NUMBER: US 60/086,586

PRIOR PLING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin version 3.1

SEQ ID NO 59

LENGTH: 537
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Publication No. US20030114370A1
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael S.
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide Fre
TITLE OF INVENTION: Thereof
FILE REFERENCE: 05213-0880 (43170-249874)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 106
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Indels:
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) ORGANISM: Homo sapiens
US-10-131-241-59
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                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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Sequence 6, Application US/10042347

Publication No US20030114370A1

GENERAL INFORMATION:

JAPPLICANT: O'Reilly, Michael S.

APPLICANT: Folkman, M. Judah

TITLE OF INVENTION: Thereoff

FILE REFERENCE: 05213-0880 (43170-249874)

CURRENT FILING DATE: 2002-01-11

PRIOR APPLICATION NUMBER: US/10/042,347

CURRENT FILING DATE: 1995-05-20

PRIOR APPLICATION NUMBER: US 60/106,343

PRIOR FILING DATE: 1998-10-30

PRIOR FILING DATE: 1998-09-16

PRIOR PELING DATE: 1998-09-16

PRIOR PELING DATE: 1998-09-16

PRIOR APPLICATION NUMBER: US 60/005,835

PRIOR PELING DATE: 1996-09-16

PRIOR PELING DATE: 1996-09-17

PRIOR APPLICATION NUMBER: US 60/005,835

PRIOR PELING DATE: 1996-09-17

PRIOR PELING DATE: 1996-09-17

PRIOR FILING DATE: 1996-09-17

PRIOR FILING DATE: 1996-09-17

PRIOR FILING DATE: 1996-09-17

NUMBER OF SEQ ID NOS: 6

SOFTWARE PELING DATE: 1996-09-17
                                                                                                                                                                                                                                                                     100 LeuGlnAspLeuTyrSerIleValArgArgAlaAspArgThrGlyValProValValAsn 119
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CORGANISM: Homo sapiens
US-10-042-347-6
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Best Local Similarity:
US-10-131-241-51
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Sequence 51, Application US/10131241

Sequence 51, Application US/10131241

Sequence 51, Application Wo. US2030012792A1

GENERAL INFORMATION:

APPLICANT: Holdaday, John W.

APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifers

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifers

TITLE OF INVENTION: Anne H.

TITLE OF INVENTION: and Regulating Amgiogenesis Using Cancer Markers

FILE REFERENCE: 05213-0344 43170-271565

CURRENT APPLICATION NUMBER: US 09/413,049

PRIOR PILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR APPLICATION NUMBER: US 69/316,802

PRIOR APPLICATION NUMBER: US 60/086,586

PRIOR PILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.1

SEQ ID NO 51

LENGTH: 632
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ORGANISM: Murinae
; ORGANISM: Canine US-10-131-241-50
                                            Alignment Scores:
Pred. No.:
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Sequence 50, Application US/20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

FILE REFERENCE: 05213-0344 43170-271565

CURRENT FILING DATE: 2002-07-22

PRIOR PAPLICATION NUMBER: US 09/413,049

PRIOR PELING DATE: 1999-05-21

PRIOR PELING DATE: 1999-05-21

PRIOR PELING DATE: 1999-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50

LENGTH: 552

TYPE: DNA
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Matches:
Conservative:
Mismatches:
Indels:
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176.00
100.00%
100.00%
76.52%

; LOCATION: (1)..(552)
; OTHER INFORMATION: Endostatin
US-10-292-418-34

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Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Sequence 45, Applisequence 97, Applisequence 14, Applisequence 14, Applisequence 186155, Sequence 285764, Sequence 221236, Sequence 21455, Sequence 21455, Sequence 147953, Sequence 147954, Sequence 124065, Sequence 2, Appliseguence 4, Appliseguence 2, Applisegu
                                                                              Sequence 4, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 30, Appli
Sequence 1178, Appli
Sequence 1178, Appli
Sequence 144, Appli
Sequence 48, Appli
Sequence 48, Appli
Sequence 48, Appli
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Sequence 1406, Ap
Sequence 3, Appli
Sequence 174961,
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Seguence 12, Appl
Seguence 4, Appli
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Sequence 3, Appli
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Sequence 3, Appl
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APPLICANT: Lo, Yue
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION: Immunofusins
TITLE OF INVENTION: Immunofusins
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/383,315
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
4 US-10-131-241-50

4 US-10-131-241-51

4 US-10-042-347-6

4 US-10-042-347-4

5 US-10-131-241-59

4 US-10-131-241-59

4 US-10-131-241-53

3 US-09-288-107-2178

4 US-10-080-797-2

3 US-09-880-107-1178

4 US-10-131-241-48

5 US-09-775-312-3

8 US-09-775-32-387-4

1 US-09-775-32-387-4

1 US-10-080-797-4

1 US-10-080-632-262492

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US-10-080-782-282-282492

US-10-080-778-971-4
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US-10-092-154-1406
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, Sequence 34, Application US/10292418
; Publication No. US20030139365A1
; GENERAL INFORMATION:
          NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 552
TYPE: DNA
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10989
      Sequence 34, Appl
                                                                                                                                      , Search time 906.667 Seconds (without alignments) 567.713 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                          230
1 PWRADDILAGPPRLLDPQPY......CRHAFVVLCIENSVMTSFSK 230
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'/ cgn2_6/ptodata1/1/pubpna/US07_NEW_PUB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US06_NEW_PUB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US06_PUBCOMB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US06_PUBCOMB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US08_NEW_PUB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US08_PUBCOMB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US08_PUBCOMB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US08_PUBCOMB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US08_PUBCOMB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US09_PUBCOMB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US09_NEW_PUB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US09_NEW_PUB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US09_NEW_PUB.seq:*
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'/ cgn2_6/ptodata1/1/pubpna/US60_NEW_PUB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US60_NEW_PUB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US60_NEW_PUB.seq:*
'/ cgn2_6/ptodata1/1/pubpna/US60_NEW_PUB.seq:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                      OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.5 552 12 US-10-292-418-34
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60.0
7.0
7.0
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                                                                                                                                          August 18, 2003, 02:40:12
                                                                                                                                                                                                                                                                                                                                       , Ygapext
, Fgapext
, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Score Match Length DB ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                    US-09-938-391-2
                                                                                                                                                                                                                                                                                                                   Xgapop 60.0 ,
Ygapop 60.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Word size:
                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                            Run on:
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Search completed: August 18, 2003, 03:43:58 Job time : 89.6667 secs
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Patent No. 6492153
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1043
CURRENT APPLICATION NUMBER: US/09/759,359A
CURRENT FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                COMPESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
CCTTY:
BASINGTON
STATE:
CCTTY:
CCMPUTRY:
CCMPUTRY:
COMPUTRY:
COMPUTR:
COMPUTER:
COMPUT
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: CARRAWAY, KERMIT L.
APPLICANT: CAROTHERS CARRAWAY, CORALIE A.
APPLICANT: FREGIEN, NEVIS L.
ITILLE ON CONCOGENE PRODUCT LIGAND
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2482 GTACACACACACACACACACACACACAG 2508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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100.00%
3.91%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-759-359A-3/c
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LENGTH: 90541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                   37088 GTACACACACACACACACAA 37062
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                                                        760
9.00
100.00%
100.00%
3.91%
                                                                       Score:
Percent Similarity:
Best Local Similarity:
Query Match:
, ORGANISM: Human
US-09-759-359A-3
                                         Alignment Scores:
Pred. No.:
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RESULT 14
US-08-179-481-1
; Sequence 1, Application US/08179481
; Patent No. 5624816
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3.91%
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Wang, Zhiwei
John Tillinghast
10.00%
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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
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hao, Qing A.
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                                                                                                                                                  110 AlaAspArg 112
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US-09-620-312D-1012
                                                                                                                                                                                                                                                                                                                                                                                                                       Wehrman, Tom
Xue, Aidong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou, Ping
Ma, Yunqing
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Query Match:
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LOCATION: (16
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APPLICANT:
 Query Match:
DB:
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                                                                                                                                                                                                                                                                                     90 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArg 109
                                                                                                                                                                                                                                                                                                                   151 GCCACCTTCCGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATCGTGCGCCCGT 210
                 OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Squence 1, Application US/08159784

| Patent No. 5643783 |
| Patent No. 5643783 |
| GENERAL INFORMATION: |
| APPLICANT: Bjorn R. Olsen |
| TITLE OF INVENTION: |
| NUMBER OF SEQUENCES: 9 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Fish & Richardson |
| STREET: 225 Franklin Street |
| CITY: Boston |
| STREET: Assachusetts |
| COUNTRY: U.S.A. |
| COMPUTER READABLE FORM: |
| MEDIUM TYPE: 3.5" Diskette, 1.44 Mb |
| COMPUTER: IBM PS/2 Model 502 or 555X |
| OPERATING SYSTEM: MS-DOS (Version 5.0) |
| SOFTWARE: WordPerfect (Version 5.1) |
| CURRENT APPLICATION DATA: |
| CHARLICATION DATA: |
| CHARLICATION NUMBER: US/08/159, 784 |
| CHARLICATION NUMBER: US/08/159, 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4031
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATJOAND. JOHN. F. Ereeman REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00246/170001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                     Gaps:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    211 GCTGACCGG 219
                                                                                                                                                                                                                                                                                                                                                   110 AlaAspArg 112
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                                                  NAME/KEY: CDS
LOCATION: (1)..(573)
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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                 US-09-561-499-12
                                                                                                                   Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-159-784-1
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 FEATURE:
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                                                                                                                                   Pred. No.:
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Sequence 12, Application US/09561526

Batent No. 6416758
GENERAL INFORMATION
ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Breken
TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.00286
CURRENT PELING DATE: 2000-04-28
FRIOR PILING DATE: 1999-04-28
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOUTHAND SEQ ID NOS: 44
SOUTHAND SEQ ID NOS: 45
SEQ ID NO 12
LENGTH: 573
                                             90 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerlleValArgArg 109
                                                                                      210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 GlyThrPheArgAlaPheLeuSerArgLeuGlnAspLeuTyrSerIleValArgArg 109
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Sequence 12, Application US/09561499
Sequence 12, Application US/09561499
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: PAIL B. Thorpe
TITLE OF INVENTION: ANTIDON METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002582
CURRENT APPLICATION NUMBER: US/09/561,499
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
1 LOCATION: (1)..(573)
US-09-561-526-12
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Matches:
Conservative:
Mismatches:
Indels:
        US-09-938-391-2 (1-230) x US-09-561-108-12 (1-573)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-391-2 (1-230) x US-09-561-526-12 (1-573)
                                                                                    151 GCACCTTCCGGGCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.57e-13
23.00
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 573
                                                                                                                           110 AlaAspArg 112
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Best Local Similarity:
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Pred. No.:
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US-09-561-526-12
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APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY
CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584.
CURRENT APPLICATION NUMBER: 06/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATERING UNCE: 2.0
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APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIHEDY COMPOSITIONS. FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002500
CURRENT APPLICATION NUMBER: US/09/561,500
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTHARE: PARCHING DATE: 200
                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: OLIGONUCLEOTIDE
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Mismatches:
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Patent No. 6342221
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LOCATION: (1)..(573)
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LOCATION: (1)..(573)
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Best Local Similarity:
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US-09-561-108-12
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LENGTH: 573
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LENGTH: 573
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ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
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                                   133 GGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATCGTGCGCCGT 192
                                                                                                                                                                                  Sequence 37, Application US/08985526
Patent No. 6080728
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CARRIER:DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION:
TITLE OF AMORES:
ORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
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Matches:
Conservative:
Mismatches:
Indels:
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STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A
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APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTONEY/AGENT INFORMATION:
NAME: MCMORIOW JT., ROBERT G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-561-500-12; Sequence 12, Application US/09561500; Patent No. 648-21; Patent No. 648-21; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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APPLICANT: Neuner-Jehle, Martin
TITLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REPERENCE: 8076.2020203
CURRENT APPLICATION NUMBER: US/09/775,325
CURRENT FILING DATE: 2401-02-01
PRIOR PILING DATE: 1999-11-24
                               APPLICANT: Prats, Herve
APPLICANT: Honiger, Jiri
APPLICANT: Honiger, Jiri
APPLICANT: Honiger, Jiri
APPLICANT: Henser-John's Martin
TITLE OF INVENTION: INTRACCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.2020S01
CURRENT APPLICATION NUMBER: US/09/449,293
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Van Den Berghe, Loic
APPLICANT: Bonnel, Sebastien
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SOFWARRE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 558
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; ORGANISM: Rattus rattuŝ
US-09-449-293-3
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181 GIGGGCCGIGCCGACCGC 198
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APPLICANT: Bossard, Carine
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APPLICANT: MacDonald, Nicholas
APPLICANT: Sim, Kim Lee
TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and
TITLE OF INVENTION: Proteins and Methods of Use
FILE REFERENCE: 05213-0370
CURRENT PAPLICATION NUMBER: US/09/206,059
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
                         Sequence 4, Application US/09315689
Parent No. 6346510
GENERAL INFORMATION
APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 ValArgArgAlaAspArg 112
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 546
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              JS-09-315-689-4
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1624 GGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 1683
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                                                                 APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
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Mismatches:
Indels:
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                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIF: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09449293 Patent No. 6267954
Sequence 4, Application US/08159784
Patent No. 5643783
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                                                                                                                                                       ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INFORMATION
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100.00%
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11.30%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                   CITY: Boston
STATE: Massachusetts
                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Abitbol, Marc APPLICANT: Uteza, Yves
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117, Appl
8690, Ap
4, Appl
69, Appl
105, App
87734, App
113, App
113, App
114, App
114, App
114, App
115, Appl
116, Appl
117, Appl
117, Appl
118, Appl
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1782, Ap
17, Appl
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Requence 6, Application US/09315689

Retent No. 6346510

GENERAL INFORMATION:

APPLICANT: Follwan, Judah

APPLICANT: O'Reilly, Michael

TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions

FILE REFERENCE: 05213-0229

CURRENT FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0
                                                                                      Sequence
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US-08-750-064-3

US-08-750-064-3

US-08-245-196B-16

US-09-222-177A-41

US-09-222-177A-41

US-09-222-177A-28

US-09-222-177A-28

US-09-222-177A-31

US-09-438-906-12

US-09-438-906-12

US-09-736-478-31

US-09-736-478-31

US-09-736-478-31

US-09-736-489-4

US-09-736-489-4

US-08-384-489-4

US-09-252-991A-8690

US-09-252-991A-8690

US-09-252-991A-8690

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US-09-222-938A-68
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Conservative:
Mismatches:
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US-09-312-283C-246
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Best Local Similarity:
        Alignment Scores:
Pred. No.:
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Query Match:
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-MODEL=frame+_p2n.model -DEV=xlp
-Q=/Cqn2_1/USPTO spool p/USO9938391/runat_04082003_130739_27621/app_query.fasta_1.718
-DB=1S8U6d_parents_NA -QFWT=fastap -SUFFIX=p2noli.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITG=bits -STRAT=1 -END=-1. THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-UNTY=pto -NORM=ext. +DEMSEIZE=500 -MINLEN=0 -MAXLENE=200000000
-USER=US09938391_@CGN 1 1133_@runat_04082003_130739_27621 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NGG_SCORES=0 -WAIL -SPBLOCK=100 -LONGLOG
-NG TIMEOUT=120 -WARN_TIMFOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAFOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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Sequence 4, 1
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/Aa_COMB.seq:*
/cgn2_6/ptodata/2/ina/BcCOMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                           nucleic search, using frame_plus_p2n model
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US-09-315-689-4
US-09-206-059-30
US-08-159-784-4
US-09-449-293-3
US-09-561-506-37
US-09-561-506-12
US-09-561-56-12
US-09-561-26-12
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Maximum DB seq length: 200000000
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Perfect score:
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Jatabase

Result Š

Word size:

Sequence:

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P-PSDB; AAB30493
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Preparation of soluble recombinant endostatin involves transforming Streptomycete host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader peptide

Example 1; Fig 6; 57pp; English

The present sequence encodes human endostatin. The protein is expressed in Streptomyces. Leader sequences of Streptomyces sp. strain C5 SnpA and S. venezuelae alpha amylase proteins are linked to the SnpA and S. venezuelae alpha amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer. Inhibition of tumour growth, inhibition of angiogenesis, isolation of receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation for cultivation in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced. 

Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;

552 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 5.21e-15 26a00 100.00% 100.00% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores:

US-09-938-391-2 (1-230) x AAC62023 (1-552)

87 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 106 엄 ò

107 ValArgArgAlaAspArg 112

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181 Grececereceacec. 198

Search completed: August 18, 2003, 00:50:02 Job time : 274.778 secs

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extrapapillary hamartoma of the retinal pigmented epithelium,
fundus flavimaculatus, idiopathic, macular hole, malignant
melanoma, membranproliferative glomerulonephritis (type II),
metallic intraocular foreign body, morning glory disc syndrome,
cmultiple evanescent white-dot syndrome, neovascularisation of ora
serrata, operating microscope burn, optic nerve head pits,
photocoagulation, punctate inner choroidopathy, rubella,
csarcoidosis, esrpiginous or geographic choroiditis, cuberculosis, Vogt-Koyanagi-Harada syndrome, diabetic retinopathy,
cuberculosis, Vogt-Koyanagi-Harada syndrome, diabetic retinopathy,
non-diabetic retinopathy, brain vein occlusion, central retinal
vein occlusion, retinopathy, in premature infants, rubeosis iridis,
neovascular glaucoma, perifoveal telangiectasis, sickle cell
cetinitis pigmentosa, retinal vasculitis, Von Hippel
Lindau disease, radiation retinopathy, retinal cryoinjury,
retinitis pigmentosa, retinochoroidal coloboma, corneal
correction preservants and frame (1) corneal ulcers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interferon-inducible protein; platelet factor 4; anti-anglogenic; anti-tumor; multifunctional protein; anglogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregory SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 551 BP; 83 A; 195 C; 179 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                          keratoplasty, pterigyia and trauma (all claimed).
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 GTGCGCCGTGCCGACCGC 197
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100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID 50 of WO9916889.
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Klein BK, McKearn JP;
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DB:
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The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, artiferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an engagenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthitis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, production of tumor calls (characteristic of lung, breast, ovarian, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor. Growth. The present sequence is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of human endostatin encoded by plasmid pMALCH#15.
multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces sp. strain C5; SnpA; S. venezuelae; alpha-amylase; endostatin; cancer; tumour growth; angiogenesis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552
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Mismatches:
Indels:
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Matches:
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                                                                           Disclosure; Page 85; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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26.00
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11.30%
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/*tag=
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Pred. No.:
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                              diseases
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DB:
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RESULT 12 ABA0077

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The present sequence is a partial coding sequence for human endostatin. A claimed method for the treatment of ocular neovascularisation, especially choroidal neovascularisation, involves increasing the level of endostatin in ocular tissue, especially where the endostatin is encoded by the present sequence, or is its fragment, derivative or variant. The increase is effected by administering a viral vector, especially an adenovirus, adeno-associated virus, a retrovirus or lentivirus vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising an endostatin-encoding nucleic acid. Cells secreting endostatin may be encapsulated and implanted within an individual. The method is used when ocular neovascularisation is caused by histoplasmosis, pathological myopia, angloid streaks, anterior ischaemic optic neuropathy, bacterial endocarditis, Best's disease, bidshor tetinochoroidopathy, choroidal haemangioma, choroidal naevi, choroidal nonperfusion, choroidal osteomas, choroidal rupture, choroideraemia, chronic retinal detachment, coloboma of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increasing the amount of endostatin in ocular tissues of afflicted individuals to a choroidal neovascularization inhibiting level -
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/partial
/product= "Endostatin"
/transl_except= "(pos:2..3,aa:His)"
/*^re= "the CDS does not include a start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Endostatin; human; ophthalmological; ocular neovascularisation;
choroidal neovascularisation; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating or preventing choroidal neovascularization comprises
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dixon KH;
                                      US-09-938-391-2 (1-230) x ABA00774 (1-549)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               Human endostatin coding sequence.
                                                                                                                                                                                 181 GTGCGCCGTGCCGACCGC 198
                                                                                                                                                                                                                                                                             ABQ81193 standard; cDNA; 551 BP
                                                                                                                                                           107 ValArgArgAlaAspArg 112
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
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                                                                                                                                                                                                                                                                                                                                                        05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-2002
                                                                                                                                                                                                                                                                                                                    ABQ81193;
                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                            ABQ81193
                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                             임
                                                                                             121 GGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes endostatin. Endostatin is a 20 kD C-terminal fragment of collagen XVIII that inhibits angiogenesis. The endostatin coding sequence may be used in the recombinant viral vector of the invention for obtaining angiostatin activity. The vector comprises a promoter capable of expressing human angiostatin operably linked to a structural gene encoding one or more domains of human angiostatin. The vector, which may be a replication defective viral vector, is useffor inhibiting angiogenesis in a mammal, especially with cancer or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant viral vector expressing human angiostatin useful for inhibiting angiogenesis in a mammalian subject with cancer or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: This sequence is given incorrectly in the sequence listing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mendez M;
                                                                                                                                                                                                                                                                                                                                                                                                           Gene; human; plasminogen; angiostatin; neovascularisation;
kringle domain; cell proliferation; viral vector;
replication-defective; cancer; tumour; ss.
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Matches:
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Indels:
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/*tag= a
/product= "Endostatin"
                  US-09-938-391-2 (1-230) x AAS00867 (1-549)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Human endostatin coding sequence.
                                                                                                                                                             181 GTGCGCCGTGCCGACCGC 198
                                                                                                                                                                                                                                                        BP
                                                                                                                                    107 ValArgArgAlaAspArg 112
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05-APR-2002; 2002US-370634P.
                                                                                                                                                                                                                                                                                                                                      (first entry)
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Query Match:

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activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including heamangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatorid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibrache neovascularisation, telangiectasia, haemophiliac joints, angiotibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and chypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a cDNA encotaing human endostatin used in the construction of immunofusin containing human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin gamma (1gG) Fc fragment.

Note: This sequence is stated in claim 12 as being amino acid sequence of plasminogen fragment, however, the rest of the specification refers to this sequence as being nucleotide sequence of human endostatin.
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product= "Endostatin(TM) C-terminus minus 3"
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The sequence encodes Human Endostatin(TW). The new method of the invention is useful for producing, recovering and purifying Endostatin convention is useful for producing, recovering and purifying Endostatin culture media, and fermentation media. Endostatin(TW) is useful for treating angiogenesis mediated diseases such as solid tumours, blood corner tumours, leukemmias, tumour metastases, benign tumours, blood borne tumours, leukemmias, tumour metastases, benign tumours, e.g. corneal schematic arthritis, psoriasis, coular angiogenic diseases, e.g. diabetic retinopathy, retinopathy of prematurity, macular concern trenopathy, retinopathy of prematurity, macular concern fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, cancer, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, conferent and hypertrophic sexes where a standial adhesions, atherosclerosis, of endothelial cells such as intestinal adhesions, atherosclerosis, conferedment and hypertrophic scars. Higher yields of more purified, and cologically active Endostatin(TW) are obtained by the new method.

Endostatin(TW) can be stored in buffers for extended periods of time, and also subjected to lyophilsation, while preserving biological activity.

Contrifugation of broth from fermentation steps in production is avoided, preventing unwanted potential cellular lysis and contamination with
                                                                                                                                                                                                                                                                       /note= "None of the above CDSs have start or stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumours, comprises recombinantly producing the protein using an expression system, and recovering and purifying the protein -
           /note= "Variant produced during fermentation reaction of Pichia pastoris harbouring an expression plasmid containing the present sequence"
                                                                                                                                                         reaction of Pichia pastoris harbouring an expression plasmid containing the present sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boerner RJ;
                                                                                      /*tag= c
/product= "Endostatin(TM) C-terminus minus 1"
                                                                                                                                          /note= "Variant produced during fermentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang-Murad A, Zhou X, Madsen J,
Y FR, Shepard SR, Schrimsher JL;
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/product= "Endostatin(TM)"
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Bermejo LL, Mistry FR,
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Pred. No.:
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82 A; 196 C; 178 G; 93 T; 0 other;

Sequence 549 BP;

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sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for expresses an anti-angiogenic polypeptide. An additional use comprises expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient.
                                                                                                                                                                                                                                                                            87 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 106
                                                                                                                                                                                                                                                                                            121 GGGCTGGCGGGCACCTTCCGCGCCTTCGTGCTCGCGCCTGCAGGACCTGTACAGCATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenesis inhibiting factor 1 and its derivative useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, angiogenesis inhibiting factor 1; IAF-1; tumour; antibody;
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P-PSDB; AAY90771.
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The present sequence encodes an angiogenesis inhibiting factor (I), designated IAF-1. The present invention also describes: (1) preparation of (I) and its derivative; (2) an IAF binding acceptor and its preparation; and (3) an IAF antibody. (I) is useful for preparing new bloological preparations for effectively treating various tumours and abnormal-vessel diseases. The IAF antibody is preferably a polyclonal antibody, mosaic antibody, single stranded antibody and human originated antibody.

Example 1; Fig 5; 41pp; Chinese.

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GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 106
                                                                                                                                                                        121 GGGCTGGCGGCCACCTTCCCTCGCCCTCGCCCTGCAGGACCTGTACAGCATC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -
                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antighabetic; ophthalmological; immunosuppressant; vasotropic; antighabetic; ophthalmological; immunosuppressant; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retinopathy; macular degeneration; myocardial anglogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy; ss.
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Matches:
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P-PSDB; AAY70252.
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Query Match: DB:

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dependent cancers. The polynucleotide and polypeptide sequences of this endostatin are useful for treating and diagnosis of tumours, ocular angiogenic diseases, osler-Webber syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma and wound granulation, for treatment of diseases related to accessive or abnormal stimulation of endothelial cells e.g. intestinal adhesions, atherosclerosis, scleroderma. The protein may also be useful as a birth control agent by reducing or preventing uterine vascularisation. The gene for endostatin may be isolated from cells or tissue that express high levels of endostatin, eg. tumour cells, by generating cDNA from mRNA using reverse transcriptase and then amplifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiostatin, human or murine endostatin and angiogenesis-inhibiting fusions and fragments, where the viral vector is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GGGCTGGCGGGCACCTTCCGCGCCTTCTTGCTCCTGCGCCTGCAGGACCTGTACAGCATC
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Mismatches:
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(MASI ) MASSACHUSETTS INST TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-angiogenic gene therapy vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 ValArgArgAlaAspArg 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357696/30.
P-PSDB; AAY08693.
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                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                 the DNA sequence.
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      GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 106
                                                                                                                                                                                                                                                                              109 GGGCTGGCGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes an endostatin protein which is the carboxy terminal protein of human collagen XVIII. Recombinant mouse endostatin (20 mg/kg) was administered subcutaneously to mice implanted with Lewis lung carcinomas. There was tumour mass regression non-detectable levels after 12 days of therapy due to the angiogenesis inhibitory activity of endostatin. Thus the protein is useful for treatment of angiogenesis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              el endostatin capable of inhibiting endothelial cell proliferation angiogenesis, useful for treating angiogenesis-dependent cancers as birth control agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; endothelial cell proliferation inhibitor; collagen XVIII; anaigidenesis inhibitor; anti-tumnur; cytostatic; antiporriatic; vasotropic; determetological; ophthalmological; vulnerary; antiarteriosclerotic; antidiabetic; haemostatic; contraceptive; ocular anglogenic disease; atherosclerosis; soleroderma; mycoardial anglogenesis; telangiectasia; angiofibroma; wound granulation, ds.
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        other;
                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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      79 A; 189 C; 176 G; 93 T; 0
                                                                                                                                                                      Gaps:
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                                                                                                                                                                                                                                                                                                                                   ValArgArgAlaAspArg 112
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99US-0315689.
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P-PSDB; AAY94323.
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                                                                                                        Percent Similarity:
Best Local Similarity:
        BP;
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        Sequence 537
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20-MAY-1999;
                                              Alignment Scores:
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el endostatin capable of inhibiting endothelial cell proliferation angiogenesis, useful for treating angiogenesis-dependent cancers as birth control agents
                                                                                                                              present sequence encodes an alternate functional endostatin
                                                                                                               Claim 11; Page 40; 68pp; English
                                  (CHIL-) CHILDRENS MEDICAL CENT.
99WO-US25605.
              98US-0106343.
                                                 Folkman MJ;
                                                               WPI; 2000-365617/31.
                                                                     P-PSDB; AAY94324.
                                                O'Reilly MS,
01-NOV-1999;
              30-OCT-1998;
20-MAY-1999;
                                                                                    Novel
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myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma and wound granulation, for treatment of diseases related to excessive or abnormal stimulation of endothelial ęg protein. When the human endostatin gene sequence AAA27004 is recombinantly expressed, an observable doublet of protein results, both versions of which are functional endostatin proteins. The present gene sequence encodes an endostatin variant which is the same as the protein encoded by AAA27004 minus the first four amino acids. Recombinant mouse endostatin (20 mg/Kg) was administered subcutaneously to mice implanted with Lewis lung carcinomas. There was tumour mass regression non-detectable levels after 12 days of therapy due to the angiogenesis inhibitory activity of endostatin. Thus the protein is useful for treatment of angiogenesis - dependent cancers. The polymucleotide and polypeptide sequences of this endostatin are useful for treating and diagnosis of tumours, ocular angiogenic diseases, Osler-Webber syndrome, our cells, by generating cDNA from mRNA using reverse transcriptase then amplifying the DNA sequence. cells e.g. intestinal adhesions, atherosclerosis, scleroderma. The protein may also be useful as a birth control agent by reducing or preventing uterine vascularisation. The gene for endostatin may be isolated from cells or tissue that express high levels of endostatin,

Seguence 534 BP; 77 A; 189 C; 175 G; 93 T; 0 other;

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                        Conservative:
                                 Mismatches:
        Length:
Matches:
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11.30%
                                 Similarity:
                         Percent Similarity:
Alignment Scores:
                                          Query Match:
                                  Best Local
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US-09-938-391-2 (1-230) x AAA27005 (1-534)

GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSer11e 106 109 GGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 168 87 유 ð

107 ValArgArgAlaAspArg 112 

RESULT 6

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AAS00868 standard; DNA; 537 AAS00868 

BP.

(first entry) 04-JUL-2001

Human gene fragment encoding Endostatin(TM) N-terminal mutant protein.

Human; Endostatin(TM); angiogenesis mediated disease; solid tumours; blood borne tumour; leukaemia; tumour metastasis; benign tumour;

pyogenic granuloma; rheumatoid arthritis; psoriasis; colon cancer; ocular angiogenic disease; diabetic retinopathy; macular degeneration; retinopathy of prematurity; macular corneal graft rejection, neovascular glaucoma; retrolental fibroplasia; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; mutant; ds. /hote= "Variant produced during fermentation reaction of Pichia pastoris harbouring an expression plasmid containing the present sequence" /note= "Neither of the above CDSs have start or stop haemangioma; acoustic neuroma; neurofibroma; trachoma; rubeosis; /product= "Endostatin(TM) N-terminal mutant#1" /product= "Endostatin(TM) N-terminal mutant#2' /partial Location/Qualifiers ಹ Ω codons" 1..534 /\*tag= /\*tag= Homo sapiens. Key CDS

WO200119989-A2

22-MAR-2001

14-SEP-2000; 2000WO-US25166.

14-SEP-1999;

(ENTR-) ENTREMED INC.

Boerner RJ; Chang-Murad A, Zhou X, Madsen J, y FR, Shepard SR, Schrimsher JL; Liang H, Sim KL, Chang Bermejo LL, Mistry FR,

P-PSDB; AAU00901, AAU00900. 2001-244802/25

Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumours, comprises recombinantly producing the protein using an expression system, and recovering and purifying the protein

Claim 6; Page 32; 67pp; English.

The sequence encouses numbaria bindostatining witerential acking the Niteranial 4 amino acids. The new method of the invention is useful for producing, recovering and purifying Endostatin (TW) from biological sources, such as biological fluids, tissues, cells, culture media, and fermentation media. Endostatin(TW) is useful for treating angiogenesis mediated diseases such as solid tumours, blood control tumours, leukaemias, tumour metastases, benign tumours, e.g. treating angiogenesis mediated diseases such as solid tumours, blood control to the nemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, c.g. diabetic retinopathy, retinopathy of prematurity, macular correct retrolental fibroplasia, rubeosis, osler-Webber Syndrome, cancer, retrolental for treating disease of excessive or abnormal stimulation cancer and hypertrophic scars. Higher yields of more purified, and biologically active Endostatin(TW) are obtained by the new method.

Collegically active Endostatin(TW) are obtained by the new method.

Collegically active Endostatin(TW) are obtained by the new method.

Collecting subjected to lyophilisation, while preserving biological activity.

Contribugation of broth from fermentation steps in production is avoided, particles and contaminal and contaminal production is avoided. additional proteins, pigments, enzymes and other cellular chemicals and The sequence encodes Human Endostatin(TM) N-terminal deletion debris.

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AAA27005;
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Vuori K;
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                                                                                                                                                                                                                                                                              CTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGGGCACGGCTCCGACCCCCAGCGGGCGC 384
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                                                                                                                                                                                                                                                                                                                       AlaSerSerLeuLeuAlaGlyArgLeuLeuGluGlnGlnGluAlaAlaSerCysArgHisAla 214
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                                                                                                                                                                                                                  205 GTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCG 264
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                                                                                          ValleuHisLeuValAlaLeuAsnSerProGlnProGlyGlyMetArgGlyIleArgGly
                                                                                                     25 GTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCGGGGGGCATGCGAGGCATCCGGGGA
                                                                                                                                                                                                 ValProValValAsnLeuArgAspGluValLeuPheProSerTrpGluAlaLeuPheSer
                                                                                                                              AlaAspPheGlnCysPheGlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAla
                                                                                                                                                                                                                                   GlySerGluGlyGlnLeuLysProGlyAlaArgllePheSerPheAspGlyArgAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken; cancer; inflammation; angiogenesis-dependent disease; ds.
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176
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Mismatches:
Indels:
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                Length:
Matches:
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                              Percent Similarity:
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14-JUL-1999;
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        Alignment Scores:
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GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 106
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                                                                                                                                                                                                                                           The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancers, inflammation, rheumatoid arthritis, chronic articular rheumatism, psoriasis, disorders associated with inopportune invasion of vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy of premarturity, macular degeneration, corneal graft rejection, retrolental fibroplasia, rubeosis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent diseases include Osler Webber syndrome, myocardial angiogenesis, plaque neovasculisation, telangiectasia, haemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                                 Endostatin peptide comprising at least four endostatin amino acid residues are e.g. angiogenesis inhibitors for treating cancer and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; endothelial cell proliferation inhibitor; collagen XVIII; anglogenesis inhibitor; anti-tumour; cytostatic; antipscriatic; vasotropic; determatological; ophthalmological; vulnerary; antiarteriosclerotic; antidiabetic; haemostatic; contraceptive; coular anglogenic disease; atherosclerosis; soleroderma; myocardial anglogenesis; telangiectasia; anglofibroma;
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84..534
/*tag= a /product= "Endostatin protein"
                                                                                                                                                                                            Disclosure; Page 115-116; 146pp; English.
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2001-040937/05.
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Query Match:
                             P-PSDB; AAB49381
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541 TCCTTCTCCAAG 552

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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
                                                                                                                               angiogenesis-related disorder, such as cancers or diabetic retinopathy,
                                                                                                                                                                                                                                                                                                                                                   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
                                                                                                           isolated nucleic acid molecule for the treatment of
                                                                                                                                                      encodes an endostatin protein
                                                                                                                                                                                               Claim 2; Fig 4; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endostatin coding sequence.
Tong X;
                                           2002-354068/39
                                                               P-PSDB; AAO17430.
Sheppard MG,
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Sequence 555 BP; 78 A; 203 C; 191 G; 83 T; 0 other;

Canis familiaris.

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481 GAGGCCGCGAGCTGCCGCCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC 540
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                                                                                                                                                                                                                                                                                                       ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe 126
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                                                                                                                                                                                                                                                                                                                                                                                                                     PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 166
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                                                                                                                                      HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro
            555
0 0 0 0 0 0 0
            Length:
Matches:
Conservative:
Mismatches:
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angiogeneeis; inhibitor; cytostatic; antirheumatoid; antiatrhritic; antipsoriatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastrasis; atherosclerosis; posriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogeneeis; plaque neovascularisation; telanglectasis; wound granulation; keloid scar; gene therapy; ds.
                                                                       Canine; immunoglobulin Fc fragment; endostatin; immunofusin;
                                                         angiogenesis inhibitor, endostatin DNA.
              BP.
              AAZ51309 standard; DNA; 552
                                           (first entry)
                                           06-JUN-2000
                            AAZ51309;
                                                          Canine
RESULT 3
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'note= "Does not include stop codon" "Endostatin" Location/Qualifiers 99WO-US19329 98US-0097883 (LEXI-) LEXINGEN PHARM CORP /\*tag= a /product= Li Y, Gillies SD; WPI; 2000-237616/20. WO200011033-A2 25-AUG-1999; 25-AUG-1998; 02-MAR-2000. Lo K Key

Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -

P-PSDB; AAY70265

Example 8; Pages 58-59; 68pp; English.

a signal sequence, an immunoglobulin Fc region, and an anglogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic carantomas, returnopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental confibroma, wound granulation, telangiectasia, haemophiliac joints, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encoding canine endostatin used in the construction of immunofusin containing canine The patent discloses a DNA molecule encoding a fusion protein comprising immunoglobulin Fc fragment.

Sequence 552 BP; 77 A; 204 C; 190 G; 81 T; 0 other;

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Canis familiaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGGGGCCCCCCACACGCTCCTACGTGCACTTCCAGCCCGCTCGCCCCACTGGTGGG 120
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          cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 829 BP; 124 A; 314 C; 278 G; 113 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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/*tag= a
/product= "pro-endostatin"
/partial
/note= "no start codon"
ischaemic limb angiogenesis; diabetic
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                                                              Location/Qualifiers
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                                          Canis familiaris.
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GlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeu 100
                                  LysProGlyAlaArgIlePheSerPheAspGlyArgAspValLeuGlnHisProAlaTrp
                                                                                                                                                                  301 CAGGACCTCTACAGCATCGTGCCGCCGCCGCACCGGGGTGCCCGTCGTCACCTC
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on:	August 17, 2003, 22:57:56 ; Search time 272.778 Seconds (without alignments) 2276.105 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-938-391-2 230 1 PWRADDILAGPPRLLDPQPYCRHAFVVLCIENSVMTSFSK 230	
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Searched:	2552756 segs, 1349719017 residues	
Word size:	1	
Total number of	Total number of hits satisfying chosen parameters: 5103490	
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing	Post-processing: Listing first 45 summaries	
Command line parameters:  MODEL=frame+ p2n.model Q=/cgnZ_1/USFTO spool_p -DB=N Geneseq_19Jun03 -Q -LOOPEXT=0 -UNITS=bitsLIST=45 -DOCALIGN=200OUTFWT=pto -NORM=ext -H -USER=US09938391 @CGN 1 -NO MMAD - LARGEQUERY -NE -DBV TIMEOUT=120 -WARN I -FGAPEXT=7 -YGAPOP=60 -Y	Command line parameters: -WODEL=frame+ p2n.model -DEV=xlp -WODEL=frame+ p2n.model -DEV=xlp -WODEL=frame+ p2n.model -DEV=xlp -WODEL=frame+ p2n.model -DEV=xlp -USGPO-p2n2 1/USPO-p2n01 p/US09938391/runat 04082003_130738_27574/app_query.fasta_1.718 -DB=N Geneseq_19Jun03 -OFMT=fastap -SUFFIX=p2n01i.rng -MINMATCH=0.1 -LOOPCL=0 -LLOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LLST=45 - DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGG=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -USER=US09938391 @CGN 11 605 @runat 04082003 130738_27574 -NCPU=6 -ICPU=3 -NO MAAP -LARCEGUERY -NGS GCORES=0 -WAITT -DSPBLOCK=100 -LONGLOG -DBV TIREOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6	

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10:

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

						SUMMAKLES	
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	<u>د</u> د	26		534		AAA27005	Alternate human en
	φ t	50		537		AAS00868	gene tragme
	- α	9 6		0 4 4 4 0 6		AAX77719	Human endostatin D
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	16	26		552		AAA68203	Human endostatin c
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	20	7 7 7		555		AA166529	υ _
	21	56		558		ABA99261	endostat
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	2 6	7 P		816		AAA64013	DNA encoding a hum
	30	26		900		ABK09977	Synthetic plasmid
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	2 6	9 7 2 6		1264		ABQ/6/40 DDT84484	UNA encoding numan Human alpha-1 coll
	34	<b>5</b> 6		3394		AAX78379	Human alphal (XVII
	35	56		3394		ABN95680	Gene #2178 used to
	36	56 26		4551		ABV94763	Human pancreatic c
	. 8	7 6		4875		ABO54955	Human ovarian anti
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υu	4 4 2	7 6 7 6		5/664		AAK83781 AAK83782	human immune/naema Human immune/haema
,	4.3	23		552		AAX77715	Murine endostatin
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<u> </u>	Dog; psor	Dog; pro-en psoriasis;	endostatin; ; rheumatoid	in; enc toid ar	osta	endostatin; anglogenesis; cancer; l arthritis; retinopathy; macular c	ser; gene tnerapy; lar degeneration;
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1 239 C 280 G 143 C
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                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Feng,Y., Cui,L.B. and Ma,Q.J.
Direct Submission
Submitted Submission
Submitted Sisser-2001) Genetic Engineering, Beijing Institute of
Biotechnology, Taiping Road, Beijing 100850, P.R. China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 50.7 Liu, C.X. and Ma, Q.J. Inhibition effect in vitro of purified endostatin expressed in
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Endostatin contributes to maintain cartilage homeostasis via
promotion of the anabolic program of chondrocytes
Unpublished
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Homo sapiens collagen XVIII mRNA, partial cds.
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AF282883 T86 bp mRNA linear PRI 14-JUN-2002 Homo sapiens multi-functional protein MFP mRNA, complete cds. AF282883 AF282883.1 GI:21425750
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Method of producing functional protein domains
Patent: WO 0210372-A 14 07-FEB-2002;
Applied Research Systems ARS Holding S.A. (AN)
Location/Qualifiers
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CO7KI4/56,
CO7KI4/78,CI2N9/68,CI2N15/00,A61K37/02
Fused protein containing angiostatin component and utilization
                                                                                                        BARBARA'K KLEIN, JOHN P MCKEARN
C12N15/09,A61K38/00,A61K48/00,A61P9/10,A61P35/00,C07K14/52, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotzi, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Bases I to 555)
2 (Bases I to 555)
2 (Bases I to 555)
Cloning and expression of human endostatin gene in Escherichia coli Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases I to 555)
Zhi-Yong, H., Biao, L., Wei-Jie, Z. and Xiang-Fu, W.
Direct Submission
Submitted (07-SEP-1999) Shanghai Institute of Biochemistry, Chinese Academy of Sciences, 320 Yueyang Road, Shanghai 200031, P. R. China Location/Qualifiers
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01-OCT-1997 US 60/060609
MARK A BOLANOWSKI, MAIRE H CAPARON, GERALD F CASPERSON, SUSAN
                                                                                                                                                                                                                                                                /organism='Homo sapiens (human)'. Location/Qualifiers
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Homo sapiens type XVIII collagen mRNA, complete cds.
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/note="endostatin"
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                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 552)
Bolanowski, M.A., Caparon, M.H., Casperson, G.F., Gregory, S.A., Klein, B.K. and Mokearn, J.P.
Fused protein containing angiostatin component and utilization thereof in antitumor therapy
GD SEARLE AND CO
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Angiogenesis-inhibiting peptides and proteins and methods of Patent: WO 0230982-A 2 18-APR-2002;
EntreMed, Inc. (US)
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AX473835 AX473835.1 GI:22208005
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              PAT 02-APR-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Angiostatin and endostatin binding proteins and methods of use Patent: WO 0193897-A 30 13-DEC-2001;
EntreMed, Inc. (US)
Location/Qualifiers
                                                                                                                                                  Liang, H., Sim, K.L., Chang-Murad, A., Zhou, X., Madsen, J.,
Boerner, R.J., Bermejo, L.L., Mistry, F.R., Shepard, S.R. and
Schrimsher, J.L.
Mcthod of producing and purifying endostatin?tm protein
L Patent: WO 0119989-A 4 22-MAR-2001;
EntreMed, Inc. (US)
Location/Qualifiers
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                         Liang, H., Sim, K.L., Chang-Murad, A., Zhou, X., Madsen, J., Boerner, R.J., Bermejo, L.L., Mistry, F.R., Shepard, S.R. and Schrimsher, J.L.
Method of producing and purifying endostatin?tm protein Patent: WO 0119989-A 10 22-MAR-2001;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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O'Reilly,M.S. and Folkman,M.Judah.
Therapeutic antianglogenic endostatin compositions
Patent: US 6346510-A 4 12-FEB-2002;
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Sequence 4 from patent US 6346510.
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O'Reilly,M.S. and Folkman,M.Judah.
Therapeutic antiangiogenic endostatin compositions
Patent: US 6346510-A 6 12-FRB-2002;
Location/Qualifiers
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6 from patent US 6346510.
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AITDSTQSIIYVGVKLSDLQMGKQQIIFYYTEPGSQSSYAAATFTVPTLLNQWTRFAI
SVEEDEVILYLDCEEHBRVRFERSPDBMELEEGSGLFVAQAGGADPDKYQGVIADLRL
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SGTRSSAGSPQQAERTRVEERLQVSTGGTGPKGEKGEKGERGPKGDSGTSGILGTGAT
KGEKGEKGELGIKGSAGFGYPGSKGQKGEPGEPGPPGPLSRHTDSMSLEQVTGPPGPT
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PGPPGPPGSVVYDSNNGFSDASRPAFPGFHQFPGKGEKGDVGAPGPPGQFPYDLSRF
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1 (basea 1 to 5279)
Halfter, W., Dong, S., Schurer, B. and Cole, G.J.
Collagen XVIII is a basement membrane heparan sulfate proteoglycan J. Biol. Chem. 273 (39), 25404-25412 (1998)
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481 GAGGCCGCGAGCTGCCCACGCCTTCGTGCTCTGCATCGAGAACAGCGTCATGACC 540
                                                   207 GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Losses 1 to 5279).
Halfeer,W. and Dong,S.
Direct Submission
Submission
Submitted (11-AUG-1998) Neurobiology, University of Pittsburgh, 3500 Terrace Street, Pittsburgh, PA 15261, USA
Halfeer,W. and Dong,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-AUG-2001) Neurobiology, University of Pittsburgh, 3500 Terrace Street, Pittsburgh, PA 15261, USA Sequence update by submitter
On Aug 31, 2010 this sequence version replaced gi:3493142.
Location/Qualifiers
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Gallus gallus collagen XVIII mRNA, complete cds.
AF083440
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             181 GTGCGCGCGCGCGCACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTCTTTC
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
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Patent: EP 1191036-A 3 27-MAR-2002,
Pfizer Products Inc. (US)
Location/Qualifiers
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Sequence 3 from Patent EP1191036.
AX399631
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                                                                                       661 GAGAACAGCGTCATGACCTCCTTCTCCAAG
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                                                                                                                                        Sheppard, M.G. and Tong, X. Methods and compositions for diagnosing and treating disorders involving angiogenesis Patent: EP 191036-A 1 27-MAR-2002; Pfizer Products Inc. (US)
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Sequence 1 from Patent EP1191036.
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AF018081 Homo sapi
AK322561 Homo sapi
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AL133433 Homo sapi
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AR183520 Sequence
AR217279 Sequence
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U03715 Mus musculu
IS1044 Sequence 1
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AF257775 Mus muscu
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BD128313 Endostati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AF083440
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AR193165
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BD081407
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AX370853
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/USO9938391/runat_04082003_130738_27585/app_query.fasta_1.718
-Q=/cgn2_1/USPTO_spool_p/USO9938391/runat_04082003_130738_27585/app_query.fasta_1.718
-DB=GeneEmbl -QFMT=fastap -SUFFIX=p2noli.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=0.1590 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=105938391_@CGM_1 1 5066_@runat_04082003_130738_27585 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLCK=100 -LONGLOG
-DEV_TIMEDOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
                                                                                                                     ; Search time 3661.11 Seconds (without alignments) 2570.043 Million cell updates/sec
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                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                     OM protein - nucleic search, using frame_plus_p2n model
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Delext 7.0
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Maximum DB seq length: 200000000
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Length: Matches: Conservative: Mismatches: Indels: Gaps:	(1-551)	euAsnSerProGlnProGlyGl	GTGCTGCTGGTGGTCGTCAACAGCCCGCAGTCGGGCGGCCTTGCGGGGCAT	GinAlaArgAlaAlaGly	scadececececedes	vrSeril	GACCTGTACAGCATCGTG	JASPGluValLeuPhePro	3GGACGAGGTGCTGTTTCCTAGCT	GlySerGluGlyGlnLeuLysProGlyAlaArgllePhe	SCCGGCGCCGCATCTTC	euGlnHisProAlaTrpProArgLysSerValTrpHisGl	CCAGAAGAGCGTGTGGCAC	sGluThrTrpArgThrGlu	gagacerededegac	ArgLeuLeuGluGlnGlnGlu	CTGC	'sIleGluAsnSerValMetThrSerPheSerLy	TTCATTGTCCTCTGCATCGAGAACAGCTTCATGACCTCCTCCAAG
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Search completed: August 17, 2003, 22:57:44 Job time : 2043.33 secs

304 167 364

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Bos taurus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

1 (bases 1 to 551)

Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 25-APR-2001
                                                                                                                                     GlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThrGlu 187
                                                                                                                                                                           365 GGCTCGGACCCCAGTGGCCGGAGGCTGATGGAGGTTACTGTGAGACATGGCGAACTGAA 424
                                                                                                                                                                                                                188 AlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGlnGlu 207
                                                                                                                                                                                                                                    425 ACTACTGGGGCTACAGGTCAGGCCTCCTCCTCCTGCTGTCAGGCAGCTCCTGGAACAGAAA 484
                                                                                                                                                                                                                                                                                         208 AlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThrSer 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="MARC 2BOV"
/note="Wetcor: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
 245 AGCTGGGACTCCCTGTTTTCTGGCTCCCAGGGTCAACTGCAACCGGGGCCCGCATCTTT
                                                             SerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLySSerValTrpHis
                                                                                  305 TCTTTTGACGGCAGAGATGTCCTGAGACACCCAGCCTGGCCGCAGAAGAGCGTATGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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/organism="Bos taurus"
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/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
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BACKWARD: GTTTTCCCAGTCACGACG
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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COMMENT
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                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11 (bases 1 to 715)
M1H-MGC http://mgc.nci.nih.gov/.
National institutes of Health; Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 ArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhePro 127
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                                                                                                                                                                                                                                                             Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM64 row: b column: 12
High quality sequence stop: 567.
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CBS96713
AGENCOURT_12990486 NIH_MGC_178 Mus musculus cDNA clone
IMAGE:30299651 5', mRNA sequence.
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Matches:
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Mismatches:
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Mus musculus
                                                                            CB596713.1 GI:29514569
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92.90%
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/tissue_type="epithelioid carcinoma"
/lab hose="DH10B (phage-resistant)"
/clone_lib="NHH MGC-70"
/note="Organ: pacreas; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 CACAGCCACCGCGCACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCA
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   distribution: MGC clone distribution information
            found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9704 row: d column: 16
High quality sequence stop: 688.
Location/Qualifiers
1. 707
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                                                                                                                                                                                                                                                                                                                                                                           707
154
14
13
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAGGATCTCTATAGCATCGTGCGCCGTGCTGACCGGGGGTCTGTGCCCATCGTCAAC 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAAGGACGAGGTGCTATCTCCCCAGGCTGGGACTCCCTGTTTTCTGGCTCCCAGGGTCAA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuLysProGlyAlaArg1lePheSerPheAspGlyArgAspValLeuGlnHisProAla 159
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                                                                                                                                          CCCTGGCGAGCAGATGACTCTTGGCCAACCCACCGCGCCTGCCAGACCGCCGAGCCTTAC 191
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 707)
                                                                                                                                                                                         ProGlyAlaPro---HisHisGlySerTyrValHisPheGlnProAlaArgProThrGly 39
                                                                                                                                                                                                                                                                                                                                                                                         PheGlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArg
                                                                                                                                                                                                                                                                                                                             AlaLeuAsnSerProGlnProGlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCys
                                                                                                                       ProTrpArgAlaAspAspIleLeuAlaGlyProProArgLeuLeuAspProGlnProTyr
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
       14
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   Conservative:
Mismatches:
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                                                                                     US-09-938-391-2 (1-230) x BG967333 (1-747)
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BE908201.1 GI:10402537
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Homo sapiens
 86.19%
79.52%
68.40%
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BG967333 12-JUN-2001 602833649F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4988053 5',
                                                                                                                                                                                                                         153 AspValLeuGlnHisProAlaTrpProArgLysSerValTrpHisGlySerAspProSer 172
                                                                                                                                                                                                                                                                                                                          234 GCAGCCGTGCCCATCGTCAACCTCAAGGACGAGCTGCTGTTTCCCAGCTGGGAGGCTCTG 293
                                                                                                                                       PheSerGlySerGluGlyGlnLeuLysProGlyAlaArgllePheSerPheAspGlyArg 152
                                                                                                                                                                                                                                             173 GlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThrGluAlaProAlaAlaThr 192
                                                                                                                                                                                                                                                                                                                                                                                193 GlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGlnGluAlaAlaSerCysArg 212
                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="taxon:10090"
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/clone="IMAGE:498053"
/clone lib="NCI CGAP_CO24"
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                                                                                                                                                                                   294 TICTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCACGCATCTTCTCCTTTGACGGCAAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; —Aetazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapDs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMINGO row: a column: 14
High quality sequence stop: 742.
Location/Qualifiers
                                                                113 ThrGlyValProValValAsnLeuArgAspGluValLeuPheProSerTrpGluAlaLeu
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 CACGCCTACATCGTGCTCTGCATTGAGAACAGCTTCATGACTGCC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 HisAlaPheValValLeuCysIleGluAsnSerValMetThrSer 227
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                                                 /tissee_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1:1 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 757)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
54 CAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCAGGCGGCATGCGGGGCATT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 ArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArgAlaAspArg 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9709 row: i column: 09
High quality sequence stop: 757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 GlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnProGlyGlyMetArgGlyIle
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Mismatches:
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Matches:
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-938-391-2 (1-230) x BE906253 (1-757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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258 c 2
                                                              225 MetThrSerPheSer 229
                                                                                                    595 Argacererrieree 609
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857.00
89.74%
82.05%
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Best Local Similarity:
                                                                                                                                                                                                                                             BE906253
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                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                             RESULT 11
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/karain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:13156931"
/clone="IMAGE:13156931"
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/dev_stage="months"
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/clone="Infiltrating ductal carcinoma"
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/clone="Infiltrating ductal carcinoma"
/clone="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: pCMV-SPORT6; Site_1: Sall;
/note="Organ: pCMV-SPORT6; Site_1: Sall;
/note="Organ: pCMV-SPORT6; Site_1: Sall;
/note=
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to dT.
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  distribution information can
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                  found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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163
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Mismatches:
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Gaps:
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Matches:
Clone distribution: NCI-CGAP clone
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                                                                                    MGI:1059687 -40RP from Gibco
Seq primer: -40RP from Gibco
High quality sequence stop: 4
Location/Qualifiers
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867.00
87.32%
79.51%
69.98%
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Washington University Genome Sequencing Center
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 611)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                AAGCCCGGGGCACGCATCTTCTCTCTTTGACGGCAAGGACGTCCTGAGGCACCCCCACCTGG
                                                                                                                                                                             ProGlyAlaProHisHisGlySerTyrValHisPheGlnProAlaArgProThrGlyGly
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Contact: Robert Strausberg, Ph.D.
  Gaps:
                                          US-09-938-391-2 (1-230) x AU125614 (1-715)
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AU125614 AU12264 HOmo sapiens CDNA clone NT2RM4001897 5', mRNA
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      436 AAGGACGAGCTGCTGTTTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG 495
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1538-32-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
HRI human cDNA project; 5'- & Maical Science, University of Tokyo, and
Helix Research Institute.
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Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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                                                                              496 AAGCCCGGGGCACGCATCTTCTCCTTTGACGCCAAGGACGTCCTGAGGCACCCCACCTGG
                                                                                                                      161 ProArgLysSerValTrpHisGlySerAsp-ProSerGlyArgArgLeuThr-AspSerT
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/cell_line="NT2"
/clone_lib="NT2RM4"
/note="Vector: pME18SFL3; mRNA fr
precursor cells"
a 278 c 220 g 103 t
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/db_xref="taxon:9606"
/clone="NT2RM4001897"
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AU125614.1 GI:10950330
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Genomics Laboratory
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/tissue_rivablines.//
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/note="Organ: color"/
/note="Organ: color"/
/rote="Organ: color"/
/cloned into EcoR1/KhoI sites using the following 5'
adaptpr: GGCACCAG(G). Size-selected solobp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 832)
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http://image.llnl.gov a column: 14
High quality sequence stop: 679.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
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Homo sapiens cDNA clone IMAGE:4582933 5',
into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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 LeuGlnAspLeuTyrSerIleValArgArgAlaAspArgThrGlyValProValValAsn 119
                                                                                                                                 CTGCAGGATCTCTATAGCATCGTGCGCCGTGCTGACGGGGGTCTGTGCCCATCGTCAACAA71
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arror
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2795 row: f column: 04
High quality sequence stop: 616.
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TCAGGGCAGGGCTCCCTGGAACAGAAGCTGCGAGCTGCCACAACAGGTTACATCGTCCT
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                                                  PheGlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUSSE872
AGENCOURT_10186760 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5584644 5', mRNA sequence.
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BU556872.1 GI:22907168
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120 483 140 543 160 603 180 663 200

423

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1156 row: 1 column: 13
High quality sequence stop: 800.
Location/Qualifiers
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                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 835)
Nath-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                                                                 pOTB7; Site_1: XhoI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GlnAspLeuTyrSerIleValArgArgAlaAspArgThrGlyValProValValAsnLeu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAACAGCCCCCTGTCAGGGGGCATGCGGGGGATCCGCGGGGGCCGACTTCCAGTGCTTC 328
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AGENCOURT 8414390 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6272287 5', mRNA Sequence.
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                                                                                                                                            240 GCTTCCAGCAAGCCCGAGCCGTGGGGGCTGTCGGGCACCTTCCGGGCTTTCCTGTCCTCTA 299
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Contact: Robert Strausberg, Ph.D.
Email: cagaba-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2450 row: g column: 08
High quality sequence stop: 638.
                                                                                                                          540 GTTACTGTGAGACATGGCGAACTGCAAACTACTGGGGCTACAGGTCAGGCCTCCTCCCTGC
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Homo sapiens
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIISI row: g column: 18
High quality sequence start: 23
High quality sequence stop: 808.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B1412588 874 bp mRNA linear EST 14-AUG-2001
2029046681 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5146409 5',
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (Dases 1 to 874)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Conservative:
Mismatches:
Indels:
Gaps:
JS-09-938-391-2 (1-230) x BI412588 (1-874)
                                                                                                                                                                          Mus musculus (house mouse)
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76.63%
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/mol_type="mRNA"
/db_xref="mRNA"
/db_xref="mRNA"
/db_xref="mRNA"
/db_xref="maxon:9606"
/clone="INAGE:627561"
/lab_host="mhH MGC:162"
/clone=lib="mhH MGC:162"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/XhoI sites using the following 5' adaptor: GGGAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 CCCTGGCGGGCAGATGACATCCTGGCCAGCCCCCCTCGCCCGAGCCCCAACCTAC 160
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Conservative:
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959.50
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                                                                                                                                                                                                                                                                                                       389
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 929)
MTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                     :::
------CTCTCACTTGCTCATACTCATCAGGACTTTCAGCCAGTGCTCACCTAGGTG
                                                                                                                                  AlaLeuAsnSerProGlnProGlyGlyMetArgGly1leArgGlyAlaAspPheGlnCys
                                                                                                                                                       210 GCACTGAACACCCCCTGTCTGGAGGCATGCGTGTGTCCGTGGAGAGTTTCCAGTGC
                                                                                                                                                                                                    PheGlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArg
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 ProGlyAlaPro---HisHisGlySerTyrValHisPheGlnProAlaArgProThrGly
                    CCCGGAGTTCCACATCACACACAGTTCCTATGTGCACCTGCCGCCGCCGCCCACC---
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                                                                40 GlyProValHisThrHisThrHisThrHisGlnAspPheGlnLeuValLeuWal
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information or found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCA158 row: c column: 06
High quality sequence stop: 588.
Location/Qualifiers
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BQ672290
BQ672290.1 GI:21783124
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT REFERENCE

PEATURES

LOCUS DEFINITION

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161 ProArgLysSerValTrpHisGlySerAspProSerGlyArgArgLeuThrAspSerTyr 180
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/mol_type="mRNA"

/mol_type="mRNA"

/db_xefe="texton:9606"

/clone="lb="btuitary"

/lab host="bH10B-Ton A ( T1 and T5 phage resistances)"

/clone=lib="MIH MGC_179"

/clone=lib="NIH MGC_179"

/clone=lib="Organ: bTain; Vector: pCMV-SPORT6.1; Site 1: ECORV

/destroyed); Site_2: Not1; Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon cloning

). Average insert size 1.1 kb. Library was constructed by

(Invitrogen). Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                            Email: cgapDs-remmil.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can tfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
g column: 24
High quality sequence stop: 689.
Location/Qualifiers
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187
20
4
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Matches:
Conservative:
Mismatches:
Indels:
                                                  Contact: Robert Strausberg, Ph.D.
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82.38$
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643 bp mRNA linear EST 27-NOV-2000 602046021F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4195660 5', BF385854
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/clone_lib="NCI CGAP_Light"
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Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
                                                                          694 TGTGAGA CGTGGCGGACGGAGGCTCCCTCGGCCACGGGCCTCCTCGCTGCTGGGG
                                                                                                                                201 GlyArgLeuLeuGluGluGluAlaAlaSerCysArgHisAlaPheValValLeuCysIle
                                                     181 CysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAla
                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ProfrpArgAlaAspAspIleLeuAlaGlyProProArgLeuLeuAspProGlnProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9531 row: i column: 05 High quality sequence stop: 761.
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Conservative:
Mismatches:
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in quality sequence stop: 761.
Location/Qualifiers
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/mol type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
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                                                                                                                                                                                                               221 GluAsnSerValMetThrSer 227
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Mus musculus
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Best Local Similarity
Query Match:
DB:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

; Search time 2038.33 Seconds (without alignments) 2742.451 Million cell updates/sec 1 PWRADDILAGPPRLLDPQPY......CRHAFVVLCIENSVMTSFSK 230 August 17, 2003, 19:46:50 US-09-938-391-2 1239 Title: Perfect score: Sequence: Run on:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

**BLOSUM62** 

Scoring table:

22781392 segs, 12152238056 residues Searched: 45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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EST: \*

Database

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em\_estin:\*
em\_estov:\*
em\_estov:\*
em\_estpl:\*
em\_estc:\*
em\_htc:\* em estba:\*

em\_estom:\* em\_gss\_hum:\* em\_gss\_inv:\* gb\_est1:\*
gb\_est2:\*
gb\_htc:\*
gb\_est3:\*
gb\_est4:\*
gb\_est5:\*
em\_estfun:\* em gss\_pln:\* em\_gss\_vrt:\*em\_gss\_fun:\* 116:

em\_gss\_phg:\* em\_gss\_vrl:\* gb\_gssl:\* em gss mam:\* em gss mus: rod: em\_gss\_pro: em\_gss\_rod:

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Description	05862 AGENCOUR	35854	72290	12588	73186	26580	398	37.0	561	112	962	573	82	CB596713 AGENCOURT	BF074459 221883 MA	AI326391 mm18109.x	B1904605 603168411	AAZ88198 VDISDIU.r	BIU80324 8028//U03 AV696242 AV696242	BG969001 602834938	BG072504 H3111D11-	BI247582 602960041	BU859398 AGENCOURT	BF166139 601776586	AA003030 mg50c06.r	44	772	20	177	909	67	888	3.99	115	100	5763 MW / 6906	26435 60336732	51007 60286521	23254	57187 gi80h1	14292	F384828 602046
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832 10 B1526380 B165673 904 73.0 832 10 B1526380 B15263 905 72.8 715 9 A0125614 A012561 867 69.2 757 10 BE906253 BE9062 847.5 68.4 747 12 BG967333 BG96733 847.5 66.4 715 14 CB596713 CB5967	Query         Query         Descrig           1019         82.2         881         14         CD105862         CD105862           983.5         79.4         843         10         BF38854         BF3855           949.5         77.4         929         13         BO672290         BC672           947.5         76.5         979         13         BO672186         B1412           947.5         76.5         979         13         BO673186         B1526           904         73.1         947         13         BU556870         B1656           904         73.0         832         10         B6387051         B06531           867         70.0         611         10         AM911243         AM12561           867         69.2         757         10         BE906253         BE9062           847.5         68.4         747         12         BG967333         BC9673           825         66.3         551         10         BF004459         BF00744	Query         Query         Query           1019         82.2         881         14         CD105862         CD105862           983.5         79.4         881         14         CD105862         BF38854         BF38854           959.5         77.4         929         13         BG672290         BG73858           949.5         76.6         874         12         BI41258         BG67385           90         73.1         947         13         BG673186         BG67385           90         73.1         947         13         BU556872         BU5567           90         73.0         832         10         BG387051         BU5567           90         73.0         81         10         BG387051         BU5567           867         70.0         611         10         AW911243         BG96738           87         69.2         757         10         BE908253         BG96738           835         67.4         747         12         BG90829         BG96738           823         66.4         770         10         BE908201         CB59673           825         65.8         551         1	Score March Length DB ID Descrig 1019 82.2 881 14 CD105862 983.5 79.4 8843 10 BF388854 BF3858 949.5 76.6 874 12 B1412588 947.5 76.6 874 12 B1412588 947.5 76.6 874 12 B1412588 906 73.1 947 13 B056872 906 73.0 832 10 BG38765 907 73.0 832 10 BG38765 867 70.0 611 10 AW911243 BB5065 867 69.2 757 10 BE906253 BE9067 883 67.4 707 10 BE908201 BE9087 883 66.4 715 14 CB596713 BE9087 883 66.4 715 14 CB596713 BE9087 884 66.3 851 10 BF004459 BF90744 885 66.3 851 10 BF0044605 BF3074	Score Match Length DB 1D  1019 82.2 881 14 CD105862 983.5 79.4 843 10 BF38854 BF3855 949.5 76.6 874 12 B1412588 947.5 76.5 979 13 B0672290 904 73.0 832 10 BF388672 904 73.0 832 10 BG387051 867 70.0 611 10 AW911243 BG3877 857 69.2 757 10 BE906253 BG9673 847.5 68.4 747 12 BE906253 BG9673 847.5 68.4 777 10 BE906251 BE9062 822 66.3 757 10 BF974459 BF9744 823 66.4 775 10 BF974459 BF9744 8247.5 68.4 777 12 BG96733 BG9673 825 67.4 707 12 BF974459 BF9744 827 66.3 757 10 BF974459 BF9744 828 66.4 775 10 BF974459 BF9744 829 66.3 757 10 BF974459 BF9744 820 66.3 777 777 777 777 777 777 777 777 777 7	Score March Length DB ID  1019 82.2 881 14 CD105862 983.5 79.4 843 10 BF38854 BF3855 949.5 76.6 874 12 B1412288 947.5 76.5 979 13 B0672290 904 73.0 832 10 BG387051 902 72.8 715 9 A1125614 A112561 904 73.0 611 10 AW911243 BB3876 857 69.2 757 10 BE906253 BG9673 847.5 68.4 747 12 BG96733 BG9673 847.5 68.4 747 12 BG96733 BG9673 847.5 68.4 777 10 BE906253 BG9673 869.5 65.8 748 707 10 BE908201 BE9062 889.5 65.8 748 9 AA288198 AA288198 885 65.0 897 12 B1904605 AV69654	Score March Length DB ID Descrig 1019 82.2 881 14 CD105862 983.5 79.4 8843 10 BF388854 BF38854 959.5 76.6 874 12 BI412586 949.5 76.6 874 12 BI412586 906 73.1 947 13 BU556872 906 73.1 947 13 BU556872 907 73.0 832 10 BG387051 BI5568 907 73.0 833 10 BG387051 BI5568 907 70.0 611 10 AW911243 BG9967 867 70.0 611 10 AW911243 BG9967 867 70.0 611 10 BE908201 CB5967 868.5 64.4 747 12 BG96733 BG9967 869.6 65.1 851 10 BF908201 CB5967 815.6 64.7 707 10 BE908201 CB5967 815.6 65.8 782 9 AI326391 BF9074 816.6 65.8 782 9 AI326391 AA288198 805 65.0 897 12 B1080524 AV69624 805 65.0 897 12 BI080524 AV69624	Score March Length DB ID Descrig 1019 82.2 881 14 CD105862 983.5 79.4 881 14 CD105862 949.5 76.6 874 12 BF412588 947.5 76.6 874 12 BF412588 906 73.1 885 13 B0672290 907 73.1 885 13 B067388 907 73.0 832 10 BG387051 867 70.0 611 10 AW911243 867 70.0 611 10 AW911243 867 70.0 611 10 AW911243 867 70.0 611 10 BE908253 875 68.4 777 10 BE908201 825 66.4 777 10 BE908201 825 66.3 551 10 BF074459 815.5 65.8 782 9 A128631 816.6 67.3 753 12 B1904605 809.5 65.0 897 12 B190824 809.6 65.0 897 12 B190824 809.6 64.4 755 12 B1908241 809.6 65.0 897 12 B1908241 809.6 64.4 755 12 B1908241 809.6 65.0 897 12 B1908241 809.6 64.4 755 12 B1908241 809.6 65.0 897 12 B1080524 797.6 64.4 733 10 BG072504	Score March Length DB ID  1019 82.2 881 14 CD105862 983.5 79.4 881 14 CD105862 949.5 76.6 874 12 B1412588 947.5 76.6 874 12 B1412588 947.5 76.6 874 12 B1412588 947.5 76.6 874 12 B152680 904 73.0 832 10 B538051 902 73.1 947 13 B055872 904 73.0 812 10 B538051 867 70.0 611 10 AW911243 B15268 887 69.2 757 10 BE906253 BE906388 887 69.2 757 10 BE906253 BE906388 887 66.4 777 10 BE906253 BE906388 888 66.4 707 10 BE906253 BE906388 889 66.4 705 12 B1904605 B19046 889 66.3 587 9 AA288198 B19046 809 65.0 897 12 B1904605 804 64.9 618 9 AV696242 AV696242 797.5 64.4 755 12 B1907504 B19086 804 64.1 733 12 B1907504 B120775 794 64.1 733 12 B1907504 B120775	Score Match Length DB ID  1019 82.2 881 14 CD105862 983.5 79.4 843 10 BF38854 BF3855 949.5 76.6 874 12 B1412588 947.5 76.5 979 13 B0672290 904 73.0 832 10 B1526580 904 73.0 832 10 B1526580 904 73.0 832 10 B1526580 905 73.1 947 13 B065872 904 73.0 832 10 B1526380 857 69.2 757 10 B1596253 847.5 68.4 747 12 B1696253 847.5 68.4 777 10 B1906253 847.5 68.4 777 12 B19658733 847.5 68.4 777 12 B19658733 847.5 68.4 777 12 B1966253 847.5 68.4 777 12 B1966254 847.5 68.4 777 12 B19662624 848.6 64.1 753 12 B1964505 794 64.1 755 12 B19652001 794 64.1 755 12 B19652998 849.6 63.3 944 13 B19659398 849.6 63.3 944 13 B19659398	Score         Query         Descrig           1019         82.2         881         14         CD105662         CD1056           983.5         79.4         881         14         CD105662         BP7385854         BP738585         BP738585         BP738585         BP738585         BP738585         BP738585         BP738585         BP738585         BP738585         BP738586         BP7388785         BP7388785         BP7388785         BP7388785         BP7388785         BP7388785         BP7388785         BP73878785         BP73878785         BP73878785         BP73878785         BP738787878         BP73878785         BP73878787         BP73878787         BP73878787         BP73878787         BP73878787         BP73878787         BP7387878         BP7387878         BP7387787         BP7387787         BP7387787         BP73877878         BP7387777         BP7387787         BP7387787	Querry         Querry           1019         82.2         881         14         CD105862         CD105862           983.5         79.4         843         14         CD105862         CD105862           959.5         77.4         843         13         BG672290         BF38854           949.5         76.6         874         12         BI412588         BG772186           947.5         76.5         879         13         BG672390         BG732186           906         73.1         947         13         BG672380         BG732186           907         73.1         947         13         BG56872         BG973186           907         73.1         947         13         BG56873         BG9756173           907         70.0         611         10         BM911243         AN911243         AN911243           867         70.0         611         10         BB906253         BG906253         BG906253         BG906253           87         69.2         757         10         BE906253         BG906253         BG906253         BG906253         BG906253           81         66.4         707         10         BE9062	Score March Length DB ID  1019 82.2 881 14 CD105862 983.5 79.4 881 14 CD105862 949.5 76.6 974 12 B1412598 947.5 76.6 974 12 B1412598 947.5 76.6 974 12 B1412588 947.5 76.6 974 13 B055872 904 73.0 832 10 BG387051 905 73.1 947 13 B055872 904 73.0 832 10 BG387051 867 70.0 611 10 AN911243 867 70.0 611 10 AN911243 867 69.2 757 10 BE908253 887 69.2 757 10 BE908253 887 66.4 777 12 BG9677333 BE90878 883 67.4 707 10 BE908210 BE90878 883 67.4 707 10 BE908291 BE90878 883 67.4 707 12 BG9677333 BE90878 884 66.3 551 10 BE908291 BE9084 885 66.4 715 14 CB59773 885 67.4 753 12 B1904605 886 65.0 897 7 B1904605 887 64.1 753 12 B1904605 888 67.0 897 818085398 889 65.0 897 840896242 797.5 64.4 755 12 B1904505 889 64.0 723 12 B1904509 889 65.0 897 73 12 B1904509 889 64.0 723 12 B1904509 780.5 63.0 894 13 B19085398 889 64.0 723 12 B1904509 780.5 63.0 895 70 84003309 772 62.3 720 12 B1904444 8814 63.1 894 13 B19085398 889 64.0 723 12 B1904509 780.5 63.0 895 9 AA0033030 772 62.3 720 12 B1904444 8814 63.3 894 13 B19085398 880000000000000000000000000000000000	Score Match Length DB ID  1019 82.2 881 14 CD105862 983.5 79.4 843 10 BF38854 BF3855 949.5 76.5 979 13 B0672290 940.5 76.5 979 13 B0672290 940.7 74.8 835 12 B1412588 947.5 76.5 979 13 B0672890 940.7 70.0 832 10 B152680 940.7 70.0 611 10 AW911243 857 69.2 757 10 BE906253 847.5 68.4 747 12 B696733 847.5 68.4 777 10 BE906253 847.5 68.4 777 10 BE906201 822 66.3 551 10 BF074459 815.5 65.8 782 9 AN288198 815.5 65.8 879 12 B104665 809.5 65.0 897 12 B1094605 809.5 65.0 897 12 B1094605 809.6 63.3 944 13 B10853998 812.6 64.4 755 12 B1904605 809.6 63.0 915 10 BF0744444 809.7 64.4 755 12 B194605 809.6 65.0 897 12 B1094605 809.6 65.0 897 12 B1094605 809.6 65.0 897 12 B1080524 809.6 65.0 897 12 B10805398 809.6	Score March Length DB ID    1019   82.2   881   14   CD10.8662     983.5   79.4   881   14   CD10.8662     949.5   76.6   874   12   B1412588     940.7   74.8   835   13   B06713186     940.7   74.9   835   13   B06713186     940.7   74.1   947   13   B1656872     847.5   64.4   747   10   BE908253     847.5   64.4   755   10   BE908201     848.5   66.4   747   10     849.6   65.0   897   12     849.6   65.0   897   12     849.6   65.0   897   12     849.6   65.0   897   12     849.6   65.0   897   13     849.6   64.1   755   10     849.6   65.0   846   13     849.6   65.0   846   13     849.6   65.0   846   13     849.6   65.0   846   13     840.6   65.0   846   14     840.6   65.0   846   14     840.6   65.0	Score March Length DB ID    1019   82.2   881   14   CD105862     983.5   79.4   881   14   CD105862     983.5   79.4   881   14   CD105862     949.5   76.6   874   12   B1412588     949.5   76.6   874   12   B1412588     947.5   76.6   874   12   B1412588     904   73.0   835   13   B067339     867   70.0   611   10   AW911243     883.5   67.4   747   10   BE908253     847.5   68.4   747   10   BE908201     822   66.3   551   10   BE908201     823   66.4   747   707   10   BE908201     824   66.3   551   10   BC908243     825   66.3   551   10   BC908243     826   66.3   551   10   BC908201     827   68.3   581   10   BC908244     809.5   65.0   897   12   B1904605     809.6   65.0   897   12   B1908201     809.7   64.1   753   12   B1908204     809.8   64.4   753   12   B1908204     809.9   64.1   753   12   B1908204     809.9   64.1   753   12   B1908204     809.8   64.1   753   12   B1908204     809.8   64.1   753   13   B1085399     809.8   64.1   753   10   B1908399     809.8   65.0   890   13   B108530     809.8   65.0   890   13   B108530     809.8   65.0   890   13   B108530     809.8   65.0   890   13   B108520     809.8   65.0   65.0   890     809.8   65.0   65.0   890     809.8   65.0   65.0   890     809.8   65.0   65.0   890     809.8   65.0   65.0   890     809.8   65.0   65.0   890     809.8   65.0   65.0   890     809.8   65.0   65.0   890     809.8   65.0   65.0   890     809.8   65.0   65.0   890	Score         Query         Cuery           1019         82.2         881         14         CD105862         CD105862           983.5         79.4         881         14         CD105862         BR78385           959.5         77.4         929         13         BO672290         BO672290           949.5         76.6         874         12         B1412588         B0673186           947.5         76.6         874         12         B1412588         B0673186           906         73.0         835         13         B067186         B0673186           907         74.8         835         12         B1412588         B0673186           907         73.0         832         10         B638055         B141258           904         73.0         832         10         BG38005         B0578           867         70.0         611         10         AW911243         B15568           867         63.2         757         10         BE908201         B15678           87         66.4         77         12         B0692733         B15967           81         66.4         75         12	Score         Query         Cuery           1019         82.2         881         14         CD105862         CD105862           983.5         79.4         881         14         CD105862         BR53854           959.5         77.4         929         13         BP588854         BR5856           949.5         76.5         979         13         BR5672290         BR51256           947.5         76.5         979         13         BR56872         BR51256           904         73.0         872         13         BR56872         BR51256           904         73.0         947         12         BR125680         BR58887           904         73.0         812         10         BR580671         BR58887           807         70.0         611         10         AW911243         BR59673           807         63.2         757         10         BB596253         BR59673           847.5         68.4         707         10         BB596263         BR59674           82.5         66.4         707         10         BB596273         BB59673           82.6         66.4         70         10	Score March Length DB ID    1019   82.2   881   14   CD105862     983.5   79.4   881   14   CD105862     949.5   76.6   874   12   B1412588     949.5   76.6   874   13   B165872     949.5   76.6   874   13     867   70.0   611   10   AW911243     867   70.0   611   10   AW911243     867   70.0   611   10   AW911243     868.5   64.4   775   10   BE908201     869.6   874   755   10   B190408     809.5   65.0   897   12   B190408     809.5   65.0   897   12   B190408     809.6   65.0   897   12   B190408     809.6   65.0   897   12   B190408     809.6   65.0   897   13   B1905339     809.6   65.0   846   13   B194404     809.6   67.7   700   67.1     809.6   67.7     809.6   700   700   13   B190408     809.6   700   67.1   700     809.6   700   67.1   700     809.6   700   67.1   700     809.6   700   700     809.6   700   700     809.6     809.6   700     809.6     809.6   700     809.6     809.6	Score March Length DB ID    1019 82.2 881 14 CD105862   983.5 79.4 881 14 CD105862   949.5 76.6 972 13 B0672290   949.5 76.6 974 12 B1412588   947.5 76.6 974 12 B1412588   967.2 74.8 835 13 B0673186   968.7 74.8 835 10 B6387051   968.7 74.8 835 10 B63887051   968.7 70.0 611 10 AW911243   867.7 70.1 BE908201 BE908283   847.5 68.4 747 77 10 BE908201 BE908283   847.5 66.4 747 77 10 BE908201 BE	Score March Length DB ID    1019 82.2 881 14 CD105862   983.5 79.4 881 14 CD105862   949.5 76.6 874 12 B1412588   947.5 70.0 611 10 AW911243   847.5 66.4 777 10 BE908201   847.5 66.4 777 10 BE908201   847.5 66.4 777 10 B1908201   847.5 66.4 777 12 B1908201   847.5 66.4 773 10 B1908201   847.5 67.0 611 10 B1908201   847.5 67.0 611 10 B1908201   847.5 67.0 67.0 67.0 67.0 67.0 67.0 67.0 67.0	Score March Length DB 1D  1019 82.2 881 14 CD105862 983.5 79.4 881 14 CD105862 949.5 76.5 979 13 B0672290 940.5 76.6 874 12 B1412588 947.5 76.5 979 13 B0672290 940.7 74.8 832 10 B1526580 940.7 70.0 611 10 AN911243 857 69.2 757 10 BE906253 847.5 68.4 777 10 BE906253 847.5 66.4 715 12 BG96701 869.5 66.3 857 10 BE906263 869.5 66.3 857 10 BE906263 869.5 66.3 857 10 BE906263 869.5 66.3 858 10 B1094665 869.6 69.9 89.4 13 B1085398 869.6 69.9 89.8 89.4 13 B10868367 870.6 69.9 89.8 89.8 89.8 89.8 89.8 89.8 89	Score March Length DB ID    1019   82.2   881   14   CD105862     983.5   79.4   881   14   CD105862     949.5   76.6   874   12   B1412588     940.6   73.0   832   13   B0673186     847.5   832   13   B0673186     867   70.0   611   10   AW911243     867   70.0   611   10   AW911243     867   70.0   611   10   AW911243     868.6   777   10   BE908201     869.6   777   10   BE908201     869.6   874   777   10   BE908201     869.6   874   775   10   BE908201     869.6   874   775   10   B690824     869.6   874   773   10   B690824     869.6   874   773   10   B690824     869.6   874   773   10   B790824     869.6   879   879   870     869.6   870   870     869.6   870   870     869.6   870   870     869.7   870   870     869.8   870     869.8   870   870     869.8   870     870     870     870     870     870     870     870     87	Score March Length DB ID    1019 82.2 881 14 CD105862   983.5 79.4 881 14 CD105862   949.5 76.6 972 13 B0672290   949.5 76.6 972 13 B0672290   940.5 76.6 972 13 B0672390   940.5 76.6 972 13 B0672390   940.5 76.6 972 13 B0672390   940.5 76.6 972 14 B0672390   940.5 76.6 972 14 B0672391   940.5 76.6 972 14 B0672391   940.5 76.6 972 14 B0672391   940.5 66.7 762 14 B0672391   940.5 66.8 97 12 B1096729   940.5 66.9 972 12 B109672904   940.6 91.2 81247582   940.6 91.2 81247582   940.6 91.2 81247582   940.6 91.2 81247582   940.6 91.2 81247582   940.6 91.2 81247582   940.6 91.2 81247444   940.6 91.2 81247444   940.6 91.3 819458299   940.6 91.3 819458299   940.6 91.3 819458290   940.6 91.3 819498290	Score March Length DB ID    1019 82.2 881 14 CD10862 983.5 77.4 929 13 BP56829 949.5 76.6 874 12 B1412588 949.5 76.6 874 12 B1412588 940.7 73.0 835 13 B0672186 940.7 73.0 835 13 B0672186 940.7 73.0 835 13 B0672186 940.7 73.0 835 13 B065253 847.5 68.4 747 12 B1636253 847.5 68.4 747 12 B1636253 847.5 68.4 747 10 B1966253 847.5 68.4 747 10 B1966253 848.5 68.9 77 10 B1966253 849.5 66.3 551 10 B1966253 840.6 66.4 771 10 B1966253 840.6 66.4 771 10 B1966253 841.6 65.0 897 12 B1086254 841.6 65.0 897 12 B1086254 842.6 66.3 551 10 B1966254 843.9 944 13 B18653998 844.0 725 12 B1966254 844.0 725 12 B1966254 770.6 62.1 846 13 B19653998 844.0 723 13 B19653998 845.6 63.3 944 13 B19653998 846.1 773 10 B196624 770.6 62.1 846 13 B19653998 870.5 63.0 948 13 B1964045 770.6 62.1 846 13 B1964044 770.6 62.1 846 13 B196404 770.6 62.1 846 14 846	Score March Length DB ID    1019 87.2   881   14   CD105862     983.5   77.4   929   13   BF58854     949.5   76.6   874   12   B1412588     949.5   76.6   874   13   B141258     949.5   76.6   874   13   B141258     949.5   76.6   874   13   B141243     949.5   76.6   874   13     949.5   76.6   874   874     949.5   76.6   874   874     949.5   76.6   874   874     949.5   76.7   944   13   B141243     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.5   949.6   949     949.6   949.6     949.6   949.6   949     949.6   949.6     949.6   949.6     949.6   949.6     949.6   949.6     949.6   949.6     949.6   949.6     949.6   949.6     949.6   949.6     949.6   949.6     940.6   949.6     940.6   949.6     940.6   949.6     940.6   940.6     940	Query         Courty         Courty         Descrip           1019         82.2         881         14         CD105862         CD105862           959.5         79.4         493         10         BF35864         BF3865           959.5         76.6         874         12         B112588         BG673290           949.5         76.6         874         12         B112588         BG67326           949.5         76.6         874         12         B112588         BG67326           949.5         76.6         874         13         BG67326         BG67326           949.5         76.6         874         13         BG67387051         BG67326           940.7         70.0         611         10         AW911243         BG7677           867         70.0         611         10         AW911243         BG7677           87         70.0         611         10         BG967333         BG96773           87         66.3         747         12         BG967733         BG76773           81         66.3         77         10         BF96673         BG77744           81         67.4         77	Query         Query         Covery         Descrip           1019         82.2         881         14         CD105862         CD105862           981.5         79.4         843         10         BT958654         BF386854         BF386864         BF386864         BF386864         BF38686         BF38686

## ALIGNMENTS

EST 15-MAY-2003 CD105862. CD105862.1 GI:30759036 EST. Homo sapiens Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. CD105862 AGENCOURT 14021788 NIH\_MGC\_179 Homo sapiens CDNA clone INAGE:30365831 5', mRNA sequence. KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION RESULT 1 CD105862 LOCUS VERSION

REFERENCE

Search completed: August 18, 2003, 00:40:15 Job time: 283.444 secs

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Matches:
Conservative:
Mismatches:
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              08/608,845
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                                                                                                                                                   TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
FILING DATE: <URNOwn>
APPLICATION NUMBER: US 08/608
FILING DATE: 16-101-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCMOCTOW JT., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                               TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                              9.74e-84
831.00
92.93$
83.70$
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Query Match:
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Percent Similarity:
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US-10-292-418-17
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Sequence 17, Application US/10292418
Publication No. US20030139365A1
GENERAL INFORMATION:
APPLICANT: Lo, Kin-Ming

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APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
FILE REFERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 2002-11-12
PRIOR PLING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
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Matches:
Conservative:
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; OTHER INFORMATION: endostatin
US-10-292-418-17
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828.00
92.93%
83.15%
66.83%
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                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
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Best Local Similarity:
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67 GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
                                                                                                                           87 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
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117
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Patent No. US20020076396A1

GENERAL INFORMATION:
APPLICANT: Abitbol, Marc
APPLICANT: Menasche, Maurice
APPLICANT: Benach, Maurice
APPLICANT: Bonnel, Sebasian
APPLICANT: Bonnel, Sebasian
APPLICANT: Pannel, Sebasian
APPLICANT: Ponnel, Sebasian
APPLICANT: Ponnel, Sebasian
APPLICANT: Ponnel, Sebasian
APPLICANT: Ponnel, Martin
APPLICANT: Neuner-Johle, Martin
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Matchés:
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CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: US 09/449,293
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 558
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Best Local Similarity:
Query Match:
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Pred. No.:
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APPLICANT: Holaday, John W.

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer.

TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers

FILE REFRENCE: 05213-034 43170-271565

CURRENT PAPLICATION NUMBER: US 09/413,049

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1999-05-21

PRIOR FILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 48

LENGTH: 540
                                                                        106
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                    CCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCACGCATC
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GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
                                                                        GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                     GTGCGCCGTGCCGACCGCGCAGCCGTCGTCGTCAACCTCAAGGACGAGCTGCTGTTT
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                   61 GCGGCATGCGGGGCATCCGCGGGGCCGACTTCCAGTGCTTCCAGCAGCGCGGGCCGTG
                                                                                 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                      107 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
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Fatent No. US20020077289A1

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Sim, Kim L.

APPLICANT: Sim, Kim L.

TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and I FILE REFERENCE: 05213-0798 (43170-25933)

CURRENT APPLICATION NUMBER: US/09/873,676

PRIOR APPLICATION NUMBER: US 60/209,065

PRIOR FILING DATE: 2001-06-02

PRIOR FILING DATE: 2001-05-08

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 123

SOTTWARE: Patentin version 3.1

SEQ ID NO 30

TYPE: DNA
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US-09-873-676-30
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Pred. No.:
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19.541-53
19.56quence 53, Application US/10131241
19.64ptication No. US20030012792A1
19.64ptication Number: US/10/131,241
10.64ptication Number: US/10/131,241
10.64ptication Number: US/10/131,049
10.64ptication Number: US/10/13,049
10.64ptication US/10/13,049
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Sequence 3, Application US/10292418

PUBLICATION NO. US20030139365A1

GENERAL INFORMATION:
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Nue
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
FILE REFRENCE: LEX-006C1
CURRENT FILING DATE: 2002-11-12
CURRENT FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 3
LENGTH: 549
                                                                                                                                        HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
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CORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (1)..(549)
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Matches:
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ORGANISM: Homo sapiens
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180 TyrCysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeu 199
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                                                                     63 SerProGlnProGlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 GluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 HisThrHisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsn
                                                                                                                                                                                         Sequence 12, Application US/09998831

Sequence 12, Application US/09998831

Fatent No. US2020119153A1

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

ITILE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY

TITLE OF INVENTION: INHIBITING VEGF

FILE REFERENCE: 4001.002584

CURRENT APPLICATION NUMBER: US/09/998,831

CURRENT APPLICATION NUMBER: 09/561,108

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

LENGTH: 573
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
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156
17
15
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Matches:
Conservative:
Mismatches:
                                                                                                           US-09-938-391-2 (1-230) x US-09-998-831-12 (1-573)
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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843.00
92.02$
82.98$
68.04$
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US-09-998-831-12
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Query Match:
DB:
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US-09-998-831-12
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                                                                                                                                 APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
APPLICANT: Fortier, Anne H.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer TITLE OF INVENTION: USGNOOTH APPLICATION WINBER: US/10/131,241
CURRENT APPLICATION WINBER: US/10/131,241
CURRENT FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR APPLICATION NUMBER: US 60/086,586
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATCHTIN Version 3.1
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177
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Mismatches:
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Matches:
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                                                                                              ; Sequence 51, Application US/10131241; Publication No. US20030012792A1; GENERAL INFORMATION:
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891.00
84.83$
83.89$
71.91$
                230
              SerPheSerLys
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CORGANISM: Murinae sp.
US-10-131-241-51
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Best Local Similarity:
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                                                                  RESULT 5
US-10-131-241-51
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              227
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USC-LO-121-241-30

Sequence 50, Application US/10131241

Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.

TITLE OF INVENTION: and Requiating Angiogenesis Using Cancer Markers

TITLE OF INVENTION: and Requiating Angiogenesis Using Cancer Markers

FILE REFERENCE: 05213-034 4 41170-271565

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT FILING DATE: 1999-10-06

PRIOR PILING DATE: 1999-0-0-06

PRIOR PILING DATE: 1999-0-0-1

PRIOR PILING DATE: 1999-05-21

PRIOR PILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50

LENGTH: 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 CACGGCTCCGACCCCAGCGGGGGGCCCTGACCGACCAACTGCGAACGTGGCGGACG
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183
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Mismatches:
Indels:
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Matches:
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959.00
99.46%
77.40%
541 TCCTTCTCCAAG 552
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Best Local Similarity:
Query Match:
DB:
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US-10-131-241-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
Pred. No.:
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        APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
FILE REPERBENCE: LEX-006C1
CURRENT APPLICATION NUMBER: 2002-11-12
PRIOR FILING DATE: 1999-08-25
PRIOR PILING DATE: 1999-08-25
PRIOR PILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CACACCCACCAGGACTTCCAGCCGGTGCTGCACCTGGTGGTGGCCCTGAACAGCCCGCAGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
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Matches:
Conservative:
Mismatches:
Indels:
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959.00
99.46%
99.46%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-292-418-34
; Sequence 34, Application US/10292418
; Publication No. US20030139365A1
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1003.00
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81.50%
80.95%
PRIOR FILING DATE: 2000-10-1
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2178
LENGTH: 3394
                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; Sequence 2178, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Cockley, Joseph G.
APPLICANT: Gene Logic, Inc.
; TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer; TILE REPERENCE: 44921-5028-W0
; CURRENT APPLICATION UNMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR PILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
   4551
187
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                                 Conservative:
Mismatches:
Indels:
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    Length:
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   1.26e-103
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sequence 64, Appl
Sequence 159, Appl
Sequence 159, Appl
Sequence 5483, Ap
Sequence 97, Appl
Sequence 11, Appl
Sequence 111, Appl
Sequence 110, Appl
Sequence 7394, Appl
Sequence 7394, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 163, App
Sequence 4136, Ap
Sequence 6709, Ap
Sequence 5547, Ap
Sequence 4417, Ap
Sequence 216, App
Sequence 243061,
Sequence 243061,
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Sequence 17, Appl
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 59, Appli
Sequence 45, Appl
                                                                                                                                                          Sequence 30, Appl
Sequence 48, Appl
Sequence 3, Appli
Sequence 3, Appli
                                                                               Sequence 12, Appl
Sequence 4, Appli
Sequence 3, Appli
Sequence 53, Appli
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Sequence 51,
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APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.56
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-171-581-163
US-10-156-761-6436
US-10-156-761-6709
US-10-156-761-5547
US-10-156-761-5547
US-10-108-605-216
US-10-027-632-243061
US-10-027-632-243062
US-10-027-632-243062
US-10-027-632-140701
US-10-027-632-150126
US-09-880-107-2178
US-10-292-418-34
US-10-131-241-50
US-10-131-241-51
US-09-998-831-12
US-10-042-347-4
US-10-292-418-3
US-10-131-241-53
                                                                                                                                                                                                                                   13 US-10-036-869-37

12 US-10-222-418-17

13 US-10-080-797-4

13 US-10-080-797-4

14 US-10-042-347-6

14 US-10-131-241-45

14 US-10-131-241-45

14 US-10-131-241-45

14 US-10-060-036-4

14 US-10-060-036-4

14 US-10-060-036-7

14 US-10-050-731-872-111

14 US-10-050-731-872-111

14 US-10-050-731-872-111

14 US-10-050-731-872-111

15 US-09-731-872-111

16 US-10-050-731-872-110

17 US-09-731-872-110
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US-10-131-241-48
US-09-775-174-3
US-09-775-325-3
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Publication No. US20030073144A1
GENERAL INFORMATION:
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LENGTH: 4551
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-MODEL=frame+_p2L.model -DEV=xlp
-MODEL=frame+_p2L.model -DEV=xlp
-Q=/Cog12_1/USPTO_spool_p/US09938391/runat_04082003_130658_27206/app_query.fasta_1.718
-Q=/Cog12_1/USPTO_spool_p/US09938391/runat_04082003_130658_27206/app_query.fasta_1.718
-DE-published Applications NA -OFMT=fastap -SUFFIX=p2n.rmpb -MINMATCH=0.1
-LCOPCL=0 -LOÖPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LISF=45 - DOCALIGN=200 -THR SCORE=ECt -THR MAX=100
-MAX_LEN=200000000 -USER=US09938391_@CGN 1 1.129_@runat_04082003_130658_27206
-MAX_LEN=2000000000 -USER=US09938391_@CGN 1 1.129_@runat_04082003_130658_27206
-LONGLOG - LICUPA=3 -NO MMAP -LARGEQUERY NEG $\overline{SCORES=0} - WART -DSBEDCK=100
-LONGLOG - DEV TIMBOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPOP=L0 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1. /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2. /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
3. /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5. /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6. /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
7. /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
8. /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
9. /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
10. /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
13. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
13. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
14. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
15. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
16. /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
16. /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
17. /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
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17. /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
17. /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                 OM protein - nucleic search, using frame_plus_p2n model
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Matches:
Conservative:
Mismatches:
Indels:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-315-372-9
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2686 AAGGCTGAGGCA 2697
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Search completed: August 17, 2003, 23:00:06 Job time : 79.2222 secs

Oy 86 AlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeu 103	Db 2388 TAGCTTTTCCTGTCAATTCTG	141 LysProGlyalaArgIle	Qy         153	Qy         161ProArgLysSerVal	Oy 166TrpHisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrp 184	Qy 185 ArgThrGluala 188 :::         Db 2686 AAGGCTGAGGCA 2697	Application US/09315372 0873158 0874150 0874150 0874150 0874150 087450 0	STATE:  CITY: San Francisco  CITY: San Francisco  STATE: California  COUNTRY: United States Of America  ZIP: 94104  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compartible  COMPUTER: IBM PC compartible  COMPUTER: IBM PC compartible  SOFTWARE: Patentin Release #1.0, Version #1.30	<i>S</i>
RESULT 14 US-08-735-609-9 ; Sequence 9, Application US/08735609 ; Patent No. 594112 ; GENERAL INFORMATION:	berlain, Jeffrey S. fitano, Andrea er, Michael A. r-Singh, Rajendra igan-O'Connor, Dennis J.	; TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS; NUMBER OF SEQUENCES: 15; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Medien & Carroll, LLP; STREET: 220 Montgomery Street, Suite 2200	CITY: San Francisco STATE: California COUNTRY: United States Of America ZIP: 94104	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/WB-DOS	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NOMBER: US/08/735,609 FILING DATE: 23-OCt-1996	CLASSIFICATION: <pre>CLASSIFICATION: <pre>chassificAtion: </pre> <pre>ATTORNEY/AGENT INFORMATION: </pre> <pre>proferencement of the profession of the profes</pre></pre>	REFERENCE/DOCKET NUMBER: 40,027  REFERENCE/DOCKET NUMBER: UM-02484  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410  TELEFACIA: (415) 397-8338  INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: double MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"  SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-08-735-609-9	Alignment Scores: 0.682 Length: 3364  Pred. No.: 107.50 Matches: 57  Score: 107.50 Matches: 23  Percent Similarity: 25.45\$ Mismatches: 48  Query Match: 2.68\$ Indels: 97  DB: 2.09-938-391-2 (1-230) x US-08-735-609-9 (1-3364)	eualaglyproproargLeub rdcccccccccccaseLeub isGlySerTyrValHisPheGlnProa 

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Mismatches:
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Matches:
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2388 TAGCTTTTCCTGTÇAATTCTG---------
           REFERENCE/DOCKET NUMBER: 0.027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LEMGTH: 3364 base pairs
TYPE: nucleic acid
STRANDEDNES: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                  Conservative:
Mismatches:
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                                                                                                           US-09-938-391-2 (1-230) x US-09-315-689-6 (1-534)
   Matches:
                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States Of America ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATER: IBM PC COMPATIBLE FORM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08735609 Patent No. 5955360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
817.00
92.66%
85.88%
65.94%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
               Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-735-609-9
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                                                                                                                                                                                                                                                11 CATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTGGCACTGAACACCCCCCCTGTCT
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US-09-315-689-6

Sequence 6, Application US/09315689

Sequence 6, Application US/09315689

Patent No. 6546510

GENERAL INFORMATION:

APPLICANT: FOLKman, Judah

APPLICANT: O'Reilly, Michael

TITLE OF INVERTION THE THE PARTICE AND THE THE PREFERENCE: 05213-0229

FILE REFERENCE: 05213-0229

CURRENT APPLICATION UNMERR: US/09/315,689

CURRENT FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 6

LENGTH: 534
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Matches:
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Query Match:
DB:
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ORGANISM: Homo
                                  Alignment Scores:
Pred. No.:
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JS-08-985-526-37
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Patent No. 6080728
GENERAL INFORMATION:
TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArg11e 146
                                                                                                                                                                                                                                          PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 166
                                                                                                                                                                                                                                                                                                                  183
                                                                                         ValargargalaaspargThrGlyValProValValAsnLeuArgaspGluValLeuPhe 126
                                                                                                                                                                                                                                                               187 GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 206
                                                                                                                                                                                                                                                                                                                                                                                                               207 GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 226
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COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Connolly, Bove, Lodge, & Hutz
1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 16-JUL-1996
ATTOCNEV AGGENT INFORMATION:
NAME: MCMORTOW Jr., ROBERT G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (302) 658-9141
TELEFAX: (302) 658-5613
INFORMATION FOR SEO ID NO: 37
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerPheSerLys 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 TCTTTCTCCAAA 555
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STATE: Delaware
COUNTRY: U.S.A.
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64 GGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGCTTCCAGCAAGCCCGAGCCGTG 123
                                                                                                                             HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr 186
                                                                                                                                                                                                                                                                               ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe 126
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                  184 GTGCGCCGTGCTGACGGGGGTCTGTGCCCATCGTCAAACCTGAAGGACGAGGTCTATCT
                                                             GlualaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln
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APPLICANT: Neuner-Jehle, Martin
ITILE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.2020/SD1
CURRENT APPLICATION UNMER: US/09/775,325
CURRENT FILING DATE: 2001-02-01
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PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09775325
Patent No. 6500449
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Abitbol, Marc
APPLICANT: Utcza, Yves
APPLICANT: Bossard, Carine
APPLICANT: Van Den Bergie, Loic
APPLICANT: Van Den Bergie, Loic
APPLICANT: Parts, Herve
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Best Local Similarity:
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                                                                             HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr 186
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                  146
                                    241 CCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGTCCGCTGAAGCCCGGGGCACGCATC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Abitbol, Marc
APPLICANT: Uteza, Yves
APPLICANT: Uteza, Yves
APPLICANT: Uteza, Yves
APPLICANT: Websche, Maurice
APPLICANT: Boneard, Carine
APPLICANT: Boneal, Sebastien
APPLICANT: Boneal, Sebastien
APPLICANT: Prats, Herve
APPLICANT: Herve
APPLICANT: Neuner-Jehle, Martin
TITE OF INVENTYON: INTRACOULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076_202U501
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SSOTUMNER: Patentin Ver. 2.0
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09449293; Patent No. 6267954; GENERAL INFORMATION:
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83.70%
67.07%
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, ORGANISM: Rattus rattus
US-09-449-293-3
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Best Local Similarity:
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                                                                                                                               147 PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp
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                                                                                                                                                                                                                                                                                   421 GAGGCTCCCTCGGCCACGGGCCAGGCCTCCTCGCTGCTGGGGGGGCAGGCTCCTGGGGCAG
                                                               127 ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLySProGlyAlaArgIle
                                                                                 301 TTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCACCTGGCCCCAGAAGAGGGTGG
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107 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
                 181 GTGCGCCGTGCCGACCGCGCGCGCGTGCATCGTCAACCTCAAGGACGACGACGCTGTTTT
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Patent No. 6201104
GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas
APPLICANT: Sim, Kim Lee
TITLE OF INVENTION: Proteins and Methods of Use
TITLE OF INVENTION: Proteins and Methods of Use
FILE REFERENCE: 05213-0370
CURRENT PELICANDN UNMERE: US/09/206,059
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 30
LENGTH: 552
TYPE: DNA
CORANISM: Homo sapiens
US-09-206-059-30
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                                                              LeuTyrSerIleValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAsp
                                                                                                                             GluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysPro
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AlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAsp
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Patent No. 6346510
Regrered INFORMATION:
GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
TURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 4
LENGTH: 546
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                                                                                   203 LeuLeuGluGlnGluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsn 222
             LeuTyrSerileValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAsp 122
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12. Application US/09561499
Fatent No. 6524583
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Philip B. Thorpe
TITLE OP INVENTION:
CURRENT APPLICATION NUMBER: US/09/561,499
CURRENT APPLICATION NUMBER: 60/131,432
FRIOR PHING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 12
LENGTH: 573
                            LysSerValTrpHisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGlu
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: OLIGONUCLEOTIDE
OTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KRY: CDS
LOCATION: (1) .. (573)
US-09-561-499-12
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GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF

FILE REFERENCE: 4001.002586

CURRENT APPLICATION NUMBER: US/09/561,526

CURRENT APPLICATION NUMBER: 60/131,432

PRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0
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70 ACCCCCCTGTCTGGAGGCATGCGTGTCTCGTGGAGCAGATTTCCAGTGCTTCCAGCAA 129
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                         GluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGlyGlnLeuLysPro 142
                                           GlyAlaArgIlePheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArg 162
                                                                                                  310 GGGCCCCGCATCTTTTCTTTTGACGGCAGAGATGTCCTGAGACACCCCAGCCTGGCCGCAG 369
                                                                                                                                             LysSerValTrpHisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGlu 182
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                                                                                                                                                                                                                                                                                                                                      550 AGCTTCATGACCTCTTTCTCCAAA 573
                                                                                                                                                                                                                                                                                                                      SerValMetThrSerPheSerLys 230
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US-09-561-526-12
'Sequence 12, Application US/09561526
'Patent No. 6416758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Seguence
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843.00
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82.98$
68.04$
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US-09-561-526-12
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LENGTH: 573
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RESULT 4
US-09-561-108-12
is Sequence 12, Application US/09561108
sequence 12, Application US/09561108
sequence 12, Application US/09561108
sequence 12, Application US/09561108
general information: Thorpe
sequence 12, Application
sequence 12, Application UNBER: US/09/561,108
sequence 12, CURRENT PILING DATE: 2000-04-28
sequence 12, Application NUMBER: US/09/561,108
sequence 12, Application NUMBER: US/09/561,108
sequence 12, Application UNBER: US/09/561,108
sequence 12, Application US/09/561,108
sequence 12, Applicati
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250 GAGGTGCTATCTCCCCAGCTGGGACTCCCTGTTTTTCTGGCTCCCAGGGTCAACTGCAACCC 309
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                                                                                                          310 GGGCCCGCATCTTTTTTTTGACGCAGAGATGTCCTGAGACACCCCAGCCTGGCCGCAG
                                                                                                                                                                                                                  143 GlyAlaArgIlePheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArg
                                                                                                                                                                                    163 LysSerValTrpHisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGlu
                                                                                                                                                                                                                                                                                         ThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArg
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OTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
1 LOCATION: (1)..(573)
US-09-561-108-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No.:
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  140 LeuLysProGlyAlaArgIlePheSerPheAspGlyArgAspValLeuGlnHisProAla 159
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APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTHROPY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002500
CURRENT APPLICATION NUMBER: US/09/561,500
CURRENT APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 12
LENGTH: 573
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                                3592 GTGCAACCCGGGGCCCGCATCTTTTTTTTTTGACGCAGAGATGTCCTGAGACACCCAGCC
                                                                                                                                      8652 TGGCCGCAGAAGAGCGTATGGCACGCTCGGACCCCACTGGGCGGAGGCTGATGGAGGT
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Conservative:
Mismatches:
Indels:
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US-09-561-500-12
'Sequence 12, Application US/09561500
'Patent No. 6342219
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-561-500-12
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Conservative:
Mismatches:
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                                                                                                    COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: ISM COMPUTE: 0.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 0204
RELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELERX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                      E: Fish & Richardso
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
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79.65%
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STRANDEDNESS: single
TOPOLOGY: linear
                                           STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeu 140
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Patent No. 5643783
GENERAL INPORMATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF NUMBER OF SEQUENCES: 9
                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                           US-09-938-391-2 (1-230) x US-08-159-784-4 (1-3394)
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88.11%
81.50%
80.95%
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SEQUENCE CHARACTERISTICS
LENGTH: 3394
                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-159-784-4
                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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Appli Appli Appli

16364, A 16474, A 8962, Ap 9043, Ap 8743, Ap 1, Appli 1, Appli

13, Appl 13, Appl 11432, A 11439, A 11397, A 4, Appli

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Patent No. 5643783
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE 3
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
US-08-735-609-9

US-09-735-609-9

US-09-244-752-9

US-09-244-752-9

US-09-244-752-9

US-09-249-99-9

US-09-249-99-9

US-08-710-861-12

US-08-189-627A-12

US-08-189-627A-12

US-08-189-627A-12

US-08-189-627A-12

US-08-306-691B-18

US-08-316-691B-18

US-08-315-113-2

US-09-517-584A-3

US-09-517-584A-3

US-09-517-584A-3

US-09-517-584A-3

US-09-252-991A-16364

US-09-252-991A-9043

US-09-252-991A-862

US-09-252-991A-8743

US-08-252-991A-8743

US-08-252-991A-8743
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US-09-252-991A-11432
US-09-252-991A-11439
US-09-252-991A-11397
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US-09-252-991A-9259
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US-09-165-543-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION UMBER: US/08/159,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ATTORNEY/AGENT INFORMATION:
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       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
    FILING DATE:
                                                                                           TELEFAX:
TELEX: 2
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       Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-O=/Cqn12 1/USFPTO spool pJUS09938391/runat 04082003 130656 27125/app_query.fasta_1.718
-DB=1SSUGd_pPTO spool pJUS09938391/runat_D4082003 130656 27125/app_query.fasta_1.718
-DB=1SSUGd_pPTEPTO spool pJUS09938391/runat_D40FPTX=p2n.rni-MNMATCH=0.1 -LGOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LCOAL -OUTFWT=proof - OUTFWT=proof - OUTFWT=proof
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                                                OM protein - nucleic search, using frame_plus_p2n model
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US-08-159-784-1

US-09-561-500-12

US-09-561-108-12

US-09-561-499-12

US-09-315-69-44

US-09-315-69-44

US-09-315-689-4

US-09-449-293-3

US-09-475-325-3

US-09-985-526-37

US-09-985-526-37
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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1239
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Match Length
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Perfect score:
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Result Š

221 uAsnSerValMetThrSer 227 ||||||| 606 GAACAGCTTCATGACTGCC 624

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Search completed: August 17, 2003, 20:06:31 Job time: 283.222 secs

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201 yArgLeuLeuGluGluGluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGl 221
12-JUL-2001; 2001CN-0126113
                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                Wu M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombination virus; proliferating; tumour cell; anti-oncogene; proliferation; telomerase promoter; therapy; tumour; ds.
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        Conservative:
Mismatches:
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                                                                                                                                                                                                                                       The invention relates to a recombination virus proliferating in a tumour cell, which can express an anti-oncogene with high efficiency. The invention also relates to the method of its proliferation. A telomerase promoter controlling the transcription of at least one necessary gene for a recombination virus proliferating, can make the virus optionally proliferate in a tumour cell, which has the activity of telomerase and basically does not proliferate in a normal cell without the activity of telomerase. The recombination virus can be used in therapy of many kinds of tumours. This polynucleotide sequence represents a DNA sequence relating to the specific proliferation in a tumour cell of the invention.
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                                                                                                        A specific proliferation in a tumour cell which can express an antioncogene with high efficiency and the use of it
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Conservative:
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846.50
86.96%
78.26%
68.32%
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                                                     WPI; 2002-464081/17
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The invention relates to developing a virus with highly-effective expression of tumour vascular genesis inhibiting factor. The virus comprises a nucleotide sequence encoding the vascular genesis inhibiting factor inserted into a non-essential proliferation region of a virus gene group. The virus selectively proliferates in a tumour cell such that along with replication of virus, the nucleotide sequence copy number of the encoded vascular genesis inhibiting factor is increased. The expression of the vascular genesis inhibiting factor inhibits tumour vascular development and inhibits formation, growth and transfer of tumour. The present sequence is that of a human endostatin polynucleotide
490 GACGAGCTGCTGTTTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virus with specific reproduction in a tumour well and effective expression of tumour angiogenesis inhibitor and its construction method
                                                                                                                                                                                                                                                        ArgheuleuGluGlnGluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGlu
                                  ArglysSerValTrpHisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCys
                                                                                                                              670 GAGACGTGGCGGACGGAGGCTCCCTCGGCCACGGCCAGGCCTCCTCGCTGCTGGGGGC
                                                                                                                                                                                   GluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful to the invention.
                                                                                                                                                                                                                                                                                                                                 222 AsnSerValMetThrSer 227
                                                                                                                                                                                                                                                                                                                                                                  790 AACAGCTTCATGACTGCC 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ccccaradacacagartricacrccagagaca 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGln 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TrpArgAlaAspAspIleLeuAlaGlyProProArg-----LeuLeuAspProGlnPro 19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human polypeptide which is a potent anglogenesis inhibitor, designated KED. The KED polypeptide, kringle proteins, or a kringle derived from human tissue plasminogen activator (LPA) protein are used to inhibit angiogeneals. Kringle protein, KED or the are useful for treating tumours, as well as atherosclerosis, arthritis, retinopathy and other similar diseases. KED is also useful for the treatment of diseases such as bronchial vascular congestion, inflammatory bowel disease, adult respiratory distress syndrome, castleman's disease, psoriasis, hepatitis, aneurysm, renal disease and haemangiome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCCACGGGGGGTCTGGAAAAATTACTGCCGT---AACCCTGATGGTGATGTAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValHisThrHisThrHisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeu
                                                                                                                                                                                                                                                    composition comprising kringle derived from plasminogen and atherosclerosis, arthritis and retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; 254 G; 147 T; 0 other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 151; 163pp; English.
                                                                                                                                  (FORD-) FORD HEALTH SYSTEM HENRY
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99US-0121633.
99US-0166176.
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67.89%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 BP; 156 A; 259
                      2000WO-US04798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                    Chopp M,
                                                                                                                                                                                                                            P-PSDB; AAB08407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                        24-FEB-2000;
                                                         24-FEB-1999;
                                                                                             L8-NOV-1999;
                                                                          25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
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a signal sequence, an immunoglobulin For region, and an anglogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (ammunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, tumour metastas benign tumours including hacemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, coular angiogenic diseases of diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis, or plaque neovascularisation, telangiectasia, haemophiliac joints' angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses a DNA molecule encoding a fusion protein comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -
                                                                                                                                                                      angiogenesis; Inhibitor; cytostatic; antirheumatoid; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastasis; atherosclarosis; psoriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encoding canine endostatin used in the construction of immunofusin containing canine
                                                                                                                                                      immunoglobulin Fc fragment; endostatin; immunofusin;
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 552 BP; 77 A; 204 C; 190 G; 81 T; 0 other;
                                                                                                                Canine angiogenesis inhibitor, endostatin DNA
                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "Endostatin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Pages 58-59; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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DNA;
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/*tag=
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AAZ51309 standard;
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                                                                          06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-1998;
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                                                                                                                                                        Canine;
                                                                                                                                                                                                                                                                                                                                Canis
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Length: Matches:

1.31e-72 959.00

Alignment Scores: Pred. No.: Score:

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120
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                                                                                                                                                                                                                                                                                                                                             1 CACACCCACCAGGACTTCCAGCCGGTGCTGCACCTGGTGGCCCTGAACAGCCGCAGCCG
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                                                                                                                                                                                                                                                                                                             GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
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                                                                                                                                                                                               HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGCCGCAGCTGCCCCCCCCCCTCGTGCTCTCTCCTCCATCGAGAACAGCGTCTAGACC
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/product= "angiogenesis inhibitor KED"
     Conservative:
                             Mismatches:
Indels:
                                                                                                                                           US-09-938-391-2 (1-230) x AAZ51309 (1-552)
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                    Best Local Similarity:
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                                                                                                                                   CTGCAGGATCTCTATAGCATCGTGCGCGTGCTGACCGGGGGTCTGTGCCCATCGTCAAC 3531
                                                         199
                                                                                                                                                                                                                                                                                                                                                                             Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection, neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; plaque neovascularisation; telangiectasia; olateral; around granulation; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological;
                                                                                                                                                                                                     219
                                                                                   LeuLysProGlyAlaArgIlePheSerPheAspGlyArgAspValLeuGlnHisProAla 159
                                                                                                                        179
          119
                                              LeuArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGluGlyGln 139
                                                                                                                        TrpProArgLysSerValTrpHisGlySerAspProSerGlyArgArgLeuThrAspSer
                                                                                                                                                                                                    200 AlaGlyArgLeuLeuGluGluGluAlaAlaSerCysArgHisAlaPheValValLeuCys
          LeuGlnAspLeuTyrSerIleValArgArgAlaAspArgThrGlyValProValValAsn
                                                                                                                                                              TyrCysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeu
                                                                                                                                                                                                                                                     IleGluAsnSerValMetThrSerPheSerLys 230
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/note= "no start codon"
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                                                                                                                                                                                                                                                                                                                                                            Canine endostatin coding sequence.
                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                    standard; cDNA; 555
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P-PSDB; AAO17430.
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                                                                                                                                   The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasis, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
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107 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
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Matches:
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Best Local Similarity:
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Mouse alpha-1 collagen cDNA
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        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                            Seguence 3394 BP; 668 A; 1130 C; 1080 G; 516 T; 0 other;
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metabolism
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(first entry)

19-NOV-1997

AAT84485

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A cDNA clone (AAT84485) codes for a mouse novel type alpha-1 (XVIII) collagen (AAW26328) that is expressed in multiple organs, especially the liver, lung and kidney. It was isolated by screening murine 15.5- and 17.5-day embryo libraries with probes based on murine type XII collagen and on human alpha-1 collagen cDNA. Isolated nucleic acids can be used to express recombinant alpha-1 collagen in transformed host cells. Claimed nucleic acid (see AAT84484) coding for human alpha-1 collagen (AAW26527) can be used to treat patients suffering from diseases associated with degradation of cartilage, and for supplementing collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage
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Alpha-1 collagen; type XVIII collagen; cartilage degeneration;
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Matches:
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Mismatches:
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Gaps:
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                                                                                           Location/Qualifiers
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Best Local Similarity:
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121 ArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeu

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mammalian endostatin. The method comprises identifying a Compound
chaving atomic coordinates with non-trivial similarity to selected
having atomic coordinates with non-trivial similarity to selected
coordinates of atoms of a mammalian endostatin involves (a) providing
coordinates of atomic coordinates of compounds in a library of candidate
compounds, (b) comparing the library of atomic coordinates to the
compounds, (b) comparing the library of atomic coordinates to the
compounds, to comparing the library of atomic coordinates to the
compounds, the candidate compound on the basis of selection
criteria which include similarities between the atomic coordinates of the
confortation. The invention also describes the use of an anti-angiogenic
fragment of endostatin comprising a domain selected from a heparin
c binding domain, a receptor binding domain, and exposed on alpha-helix A
domain, and a carbohydrate recognition domain (CRD) domain. The methods
can be used for designing and selecting endostatin minics. The compounds
identified can be used for treating undesired angiogenesis, e.g. tumours
This sequence encodes human alphal(XVIII) collagen which is used in the
corrections.
                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for identifying mimetics of
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver thumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a cytostatic activity. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression,
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                                                                                                                                                        CysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAla
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                                         LysProGlyAlaArg1lePheSerPheAspGlyArgAspValLeuGlnHisProAlaTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease st disease progression; drug toxicity; drug efficacy; drug metabolism.
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/ttag= a
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                                                     GlyArgLeuLeuGluGluAlaAlaSerCysArgHisAlaPheValValLeuCysIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collagen (AAW26327) that is expressed in multiple fissues, especially liver, lung and kidney. It was isolated from a placental CDNA library using a probe based on an unidentified collagenous protein and a probe based on mouse alpha-1 cDNA clone mc19. A claimed plasmid comprising alpha-1 collagen nucleic acid and an expression control sequence can be used to express recombinant collagen in prokaryotic or eukaryotic (especially mammalian) host cells. The collagen may be used to treat a patient suffering from a disease associated with degradation of cartilage, and for supplementing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA clone (AAT84484) codes for a human novel type alpha-1 (XVIII)
                                                                                                                                                                                                                                                                                                              Alpha-1 collagen; type XVIII collagen; cartilage degeneration; ss.
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This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiostatin, human or murine endostatin and angiogenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient.
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                                                                                                                 English
            MASSACHUSETTS INST TECHNOLOGY
                                    Pawliuk RJ;
                                                                                            Anti-angiogenic gene therapy vectors
                                                                                                                 Disclosure; Page 75-76; 83pp;
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(GENE-) GENETIX PHARM INC. (MASI ) MASSACHUSETTS INST
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                                                                                                                                                                                                21 ProGlyAlaProHisHisGlySerTyrValHisPheGlnProAlaArgProThrGlyGly 40
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polyuncleotides 98% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens of ovarian antigens, antibodies against human ovarian antigens, and the use cof ovarian antigen polyuncleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and compassing to metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation.) collycystic ovary syndrome, ovarian cysts, and dysmenorkhoea), endocrine disorders infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, opphoritis and communuodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), conderesting conders, and inflammatosus of programmal, conditions (e.g., anadiovascular disorders, autoimmune ophoritis, gastrointestinal disorders, conders, conditions (e.g., anadiovascular disorders, conditions), cardiovascular disorders, conditions (e.g., anadiovascular disorders, conditions), cardiovascular disorders, conditions (e.g., anadiovascular disorders), conditions (e.g., anadiovascular disorders)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and urinary system disorders. Ovarian antigen polypeptides and polynuclectides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynuclectides identification of gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies
     neurological disorder;
cardiovascular disorder; respiratory disorder; neurological disorder gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromsome mapping; forensic analysis; antibody preparation; cytostati; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 21q22.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sic acid molecules encoding novel ovarian polypeptides, prevention, treatment and diagnosis of cancer (e.g. ), immune disorders, cardiovascular disorders and
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at ftp.wipo.int/pub/published_pct_sequences
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Query Match:

us-09-938-391-2.p2n.rng

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The present invention relates to a composition for gene therapy, comprising a DNA encoding an anti-anglogenic protein, which shows therapeutic effects on rheumatoid arthritis. The composition is useful for treating rheumatoid arthritis and the gene therapy is effective, lasting for 14 days. The present sequence is the coding sequence for human collagen XVIII. Endostatin, which consists of the C-terminal 183 residues of collagen XVIII, was used as an anti-angiogenic protein.
                                                                                                                                                                                                                                              4402 TGTGAGACGTGGCGGACGGAGGCTCCCTCGGCCACGGCCAGGCCTCCTCGCTGGCG
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/product= "Human collagen XVIII"
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                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polymeptides (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins; T cell populations and antigen presenting calls expressing the polypeptide are useful in treating pancratic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy.

Specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCAGGCGCGGGCCGTGGGCTGGCGGCCACCTTCCGCGCCTTCCTGTCTCTCCTCCTCCTGCGCCTG 4161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAACAGCCCCCTGTCAGGCGGCATGCGGGGCATCCGCGGGGGCCGACTTCCAGTGCTTC 4101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAsnSerProGlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProValHisThrHisThrHisGlnAspPheGlnLeuValLeuHisLeuValAla
                                                                                                                                                                                                                     New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly
                                                                                                                         Jiang
                                                                                                                         Hepler WT,
                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 144; 300pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4551 BP; 780 A; 1597 C; 1522 G; 652 T; 0 other;
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187
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Conservative:
Mismatches:
Indels:
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89.43%
82.38%
                    20-AUG-2001; 2001US-313999P.
27-NOV-2001; 2001US-333626P.
    2001US-305484P.
                                                                                                                         Kalos MD,
                                                                                 (CORI-) CORIXA CORP
                                                                                                                                                               WPI; 2002-627435/67
                                                                                                                                                                                                                                                                 pancreatic cancer
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Best Local Similarity:
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  12-JUL-2001;
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The present invention relates to a new method of producing a protein, such as functional protein domain, that is either C or N-terminus of the primary translational product (PTP) of a gene, where the protein has biological activity which is distinct from PTP. The method of the invention involves growing a host cell transfected with a DNA construct comprising a regulatory DNA and a DNA targeting segment. This method is useful for producing a functional protein domain of proteins such as regulatory factors, blood products and monoclonal antibodies. The method castibed in the invention allows controlled and precise modification of the host cell genome in order to produce functional protein domain (PPD). The amount of exogenous sequence to be integrated in the host cell genome itself is used. Use of the host cell genome itself is used. Use of the host cell sequence encoding FPD also provides the advantages of both eliminating equence encoding FPD also provides the advantages of both eliminating and recombination derived alteration of sequence and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             making use of the same post-transcriptional (e.g., splicing) and/or post-translational (e.g. glycosylation, phosphorylation) processes that are actually applied in vivo for the maturation of FPD. The use of a single regulatory unit eliminates the necessity of manipulating the complementary DNA coding for the PTP to isolate the segment coding for the FPD, and adapt it to the expression vector. The present nucleic acid sequence encodes the plasmid pEnd-HR#1 FPD fusion protein of the invention. The FPD fusion protein contains the mouse Ig signal peptide (mIgSP) sequence fused to exons 38-41 of the human COLIBA1 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing functional protein domain by growing host cell transfected with DNA construct having regulatory DNA and DNA targeting segment, and optionally culturing homologously recombinant cell and collecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 900 BP; 146 A; 336 C; 274 G; 144 T; 0 other
                                                                                                                                             /*tag= h
/number= 5
/note= "Human COL18A1 exon 41"
                   'note= "Human COL18A1 exon 39'
                                                                                                                                                                                                                                                                                                                                                                                               (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV. (CHAP/) CHAPMAN P W.
                                                                              /number= 4
/note= "Human COL18A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Examples; Fig 8; 116pp; English.
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'number=
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                                     559..677
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Matches:
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1.92e-77
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Best Local Similarity:
Query Match:
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330
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211 CCCTGGCGGCCAGATGACATCCTGGCCAGCCCCCTCGCCTGCCCGAGCCCCAGCCCTAC 270
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                        21 ProGlyAlaProHisHisGlySerTyrValHisPheGlnProAlaArgProThrGlyGly 40
                                                                                                                              80
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                                                 379 CTCAACAGCCCCCTGTCAGGCGGCATGCGGGGCATCCGCGGGGCCCGACTTCCAGTGCTTC
                                                                                                                                                                                                        499 CAGGACCTGTACAGCATCGTGCGCCGTGCCGACCGCGCAGCCGTGCCCATCGTCAACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAGGCTCCTGGGGCAGAGCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATT
                                                                                                                                                                              GlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeu
                                                                                                                                                                                                                                                                                                              AAGGACGAGCTGCTGTTTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG
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                                                                            ProvalHisThrHisThrHisGlnAspPheGlnLeuValLeuHisLeuValAla
                                                                                                                              LeuAsnSerProGlnProGlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPhe
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2001US-265682P.
2001US-267568P.
2001US-278651P.
2001US-287112P.
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09-FEB-2001; 2
21-MAR-2001; 2
28-APR-2001; 2
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101 GlnAspLeuTyrSerIleValArgArgAlaAspArgThrGlyValProValValAsnLeu 121 ArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeu 361 AGGGACGAGGACTCTTCCCCAGCTGGGAGCCTTATTCTCGGGCTCCGAGGCCAGCTG LysProGlyAlaArg1lePheSerPheAspGlyArgAspValLeuGlnHisProAlaTrp

GlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeu

141

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ProArgLysSerValTrpHisGlySerAspProSerGlyArgArgLeuThrAspSerTyr

481 CCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGGCGCCGCCTGACCGACAGCGTAC CysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAla

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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, nervascular glaucoma, retrolental fibroplasis, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque meovascularisation, telanglectasia, haemophiliac joints, angiofibroma, arteriovenous malformations, ischaemic limb anglogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenesis-related disorder, such as cancers or diabetic retinopathy, encodes an endostatin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 829 BP; 124 A; 314 C; 278 G; 113 T; 0 other;
                                                                                                                                   /product= "pro-endostatin"
/partial
/note= "no start codon"
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pro-endostatin coding sequence.
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                                                                                                                                                                                                                                                       24-AUG-2001; 2001EP-0307224
                                                                                                                                                                                                                                                                                     25-AUG-2000; 2000US-227924P
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                                                           Canis
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601 GGCAGGCTGCTGGAGCAGCAGAGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATC 660

ABK09977 standard; DNA; 900

RESULT 2

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(first entry)

21-MAY-2002

ABK09977;

201 GlyArgLeuLeuGluGlnGlnAlaAlaSerCysArgHisAlaPheValValLeuCysIle

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Mouse; Ig signal peptide; mIgSP; functional protein domain; FPD; primary translational product; PTP; DNA construct; regulatory DNA; DNA targeting segment; regulatory factor; single regulatory unit; monoclonal antibody; recombination-derived alteration; blood product;
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61..888
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                                                                                                                                                                                                              Synthetic plasmid pEnd-HR#1 FPD fusion DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                       human; COL18A1; gene; mutant; fusion protein; ds
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'product= "pEnd-HR#1 FPD fusion
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/note= "Human COL18Al exon 38"
364..558
/tag= f
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/note= "Human COL18A1
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Chimeric - Homo sapiens.
Synthetic.
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CCGGGGGCCCCGCACCACCACCTACGTGCACTTCCAGCCGGCTCGCCCCCACTGGTGGG

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CCGGTCCACACACACACACCCACCAGGACTTCCAGCTGGTGGTGCACCTGGTGGTGCC

ProValHisThrHisThrHisThrHisGlnAspPheGlnLeuValLeuHisLeuValAla

20 9

ProTrpArgAlaAspAspIleLeuAlaGlyProProArgLeuLeuAspProGlnProTyr

US-09-938-391-2 (1-230) x AAL46062 (1-829)

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Length: Matches: Conservative: Mismatches: Indels:

3.75e-96 1239.00 100.00% 100.00%

Similarity:

Query Match:

Best Local Score:

Percent Similarity:

Alignment Scores:

CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCCGCGCGCCTGGACCCCCAGCCCTAC ProGlyAlaProHisHisGlySerTyrValHisPheGlnProAlaArgProThrGlyGly CTGAACAGCCCGCAGCCGGGCGGCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC 240

181

61

LeuAsnSerProGlnProGlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPhe

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: Title:	August 17, 2003, 16:43:24; Search time 272.222 Seconds (without alignments) 2280.750 Million cell updates/sec US-09-938-391-2:
Sequence:	1 PWRADDILAGPPRLLDPQPYCRHAFVVLCIENSVMTSFSK 230
Scoring table:	BLOSUM62 Xgapop 10.0, Xgapext 0.5 Ygapop 10.0, Ygapext 7.0 Egapop 6.0, Fgapext 7.0 Delop 6.0, Delext 7.0
Searched:	2552756 seqs, 1349719017 residues
Total number of	Total number of hits satisfying chosen parameters: \$105512
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

N Geneseq\_19Jun03:\*

| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\*
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:\* /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT://SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:/ (SIDSI/gcgdata/genesed/geneseqn-embl/NA1988.DAT:\*/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:\*/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT: | SIDSI | gogdata/geneseq/geneseqn-embl/NA1994.DAT: | SIDSI | gogdata/geneseq/geneseqn-embl/NA1995.DAT: | SIDSI | gogdata/geneseq/geneseqn-embl/NA1996.DAT: | SIDSI | gogdata/geneseq/geneseqn-embl/NA1997.DAT: | SIDSI | gogdata/geneseq/geneseqn-embl/NA1998.DAT: /SIDS1/gcgdata/geneseq/ /SIDS1/gcgdata/geneseq/ /SIDS1/gcgdata/geneseg/ Jatabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

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SUMMARIE	AAL46062																															ALIG	i	9 BP.			sec	r a Ll r a
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                          ProGlyAlaPro---HisHisGlySerTyrValHisPheGlnProAlaArgProThrGly 39
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Sequence 3 from Patent EP1191036.
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Percent Similarity:
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1184
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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SGTFRAFLSSRLQDIYSIVRRADRGSVPINNIKDBVLSPSWDSLFSGSGGGVQPGARI
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EQKRAASCHNSIYUCERNSFTRSK"
1167 c 1268 g 723 t
3712 TACTGTGAGACATGGCGAACTGAAACTACTGGGGCTACAGGTCAGGCCTCCTCCTGCTG 3771
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LYTEPGASQTQTGASFRLPAFVGQWTHFALSVDGGSVALYVDCEEFQRVPFARASQGL
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GEBESSKSHKEDTSLLPGLPQPPVYSPPLAGGSTTEDPRTEBTEBEDANDSIGARTU
PGTGSSGAWDEAIQNPGGLIKGGWKGQKGFPGAGGSTPEDPRTEBTEBDANDSIGARTU
PGTGSSGAWDEAIQNPGGLIKGGWKQKGPFGAGGSTPGPPGAGGPVGSPNSQP
VPGAQQEPPGPQGPPGKGGTPGBDGEPOBPGEDGRPGDFQFPGDVGFRGEKG
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                                                             219
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                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (base 1 to 4031)
Oh, S.P., Kamagata, Y., Muragaki, Y., Timmons, S., Ooshima, A. and
Olsen, B.R.
                                                                                  200 AlaGlyArgleuLeuGluGluAlaAlaSerCysArgHisAlaPheValValLeuCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolation and sequencing of CDNAs for proteins with multiple domains of Gly-Xaa-Yaa repeats identify a distinct family of collagenous proteins
Proc. Natl. Acad. Sci. U.S.A. 91 (10), 4229-4233 (1994)
                                                                                                                                                                                                                                                                  MUSCOLPRO 4031 bp mRNA linear
Mouse alpha 1(XVIII) collagen mRNA, partial cds.
L22545
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/protein_id="AAA19787.1"
/db_xref="G1:511298"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3592 GTGCAACCCGGGCCCGCATCTTTTTTTTGACGGCAGAGATGTCCTGAGACACCCCAGCC 3651
  4518 TCAGGCAGGCTCCTGGAACAGAAAGCTGCGAGCTGCCACAACAGCTACATCGTCCTGTGC 4577
                                                                                                                                                                   PAT 07-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------CTCTCACTGCTCATACTCAGGACTTTCAGCCAGTGCTCCACCTGGTG 3351
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Matches:
Conservative:
Mismatches:
                                                                                4578 ATTGAGAATAGCTTCATGACCTCTTTCTCCAAA 4610
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Olsen, B.R. and Oh.S.P.
Collagen and uses therefor
Patent: US 5643783-A 1 01-JUL-1997;
                                          220 IleGluAsnSerValMetThrSerPheSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           720
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Sequence 1 from patent US 5643783.
IS1044
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Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.E., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwant, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Malek, J.A., Sodergren, B.J., Lux, Gibbs, R.A.,
Fahey, J., Helton, E., Kettemn, M., Madan, A., Koudiques, S.,
Boutfaard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J.S., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                    4802 bp mRNA linear ROD 16-APR-2003 Wis musculus procollagen, type XVIII, alpha 1, mRNA (cDNA clone IMAGE:5310177), partial cds.
                                                                                                                            3328 TCAGGCAGGCTCCTGGAACAGAAAAGCTGCGAGCTGCCACAACAGCTACATCGTCCTGTGC 3387
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                               3268 TACTGTGAGACATGGCGAACTGCAGGCTACAGGTCAGGCTCCTCCTCCTGCTG 3327
TyrCysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeu 199
                                                                                                200 AlaGlyArgLeuLeuGluGlnGluAlaAlaSerCysArgHisAlaPheValValLeuCys 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4802)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                          3388 ATTGAGAATAGCTTCATGACCTCTTTCTCCAAA 3420
                                                                                                                                                                                                220 jlegluAsnSerValMetThrSerPheSerLys 230
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Organism="Mus musculus"

/mol type="mRNA"
/mol type="mRNA"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:5310177"
/tissue type="Liver, normal. 5 month old male mouse."
/clone lib="Nucred" (GAP_Li9"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
/note="Vector: pCMV-SPORT6"
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAR Plate: 86 Row: k Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AlaLeuAsnSerProGlnProGlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCys
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                                                                                                              Location/Qualifiers
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PHRQTVSVPGPPGPPGPPGAMGASAGQVRIWATYQTMLDKIREVPEGWLIFVAER
EELYYRVRNGFRKVILLEARTALPRGTGNBVAALQPPLVQLHBGSPYTRREYSYSTARP
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LPGAKGSVGANGAGGIPGPPGASPGPKGEKGMPGSKGDLGPG
GPPGPVIYVSSEDKAIVSTPGPEGKPGAKGSPGPKGEKGMPGKGDVGRPGGEPGG
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1857 -----CTCTCACTTGCTCATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTG 2907
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Matches:
Conservative:
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Indels:
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4415. .4420
/evidence=experimental
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TPRVSPVHCLDEEDDDEDRASGDFGSGFEESSKSHKEDTSLLPGLPQPPPVTSPPLAG
GSTTEDPRTEETEEDAAVDSIGAETLPGTGSSGAWDEAIQNPGRGLIKGGMKGQKGEP
                                                                                                                                  1054 CTGCAGGATCTCTATAGCATCGTGCGCCGTGCTGACCGGGGGTCTGTGCCCATCGTCAAC 1113
                                                                                                                                                                                                           1174 CTGCAACCCGGGGCCCGCATCTTTTTTATACGGCAGAGATGTCCTGAGACACCCAGCC 1233
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                                                                                                            LeuGlnAspLeuTyrSerIleValArgArgAlaAspArgThrGlyValProValValAsn 119
                                                                                                                                                                                         LeuArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGluGlyGln 139
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                                   Direct Submission
Submitted (04-SEP-1993) Nobuhiro Abe, Okayama University Medica Submitted (04-SEP-1993) Nobuhiro Abe, Okayama University Medica School, Molecular Biology and Biochemistry; 2-5-1, Shikata-cho, Okayama, Okayama 700, Japan (Tel:81-86-223-7151(ex.2390), Fax:81-86-222-7768)
On Jun 5, 1997 this sequence version replaced gi:467516.
934 GCACTGAACACCCCCTGTCTGGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1294 TACTGTGAGACATGGCGAACTGAAACTACTGGGGCTACAGGTCAGGCCTCCTCCCTGCTG
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/note="clones NA[1,12,286,2611]"
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TITLE
JOURNAL
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/product="alpha 1(XVIII) collagen"
/protein id="AAA20657.1"
/bctein id="eq1:48773.1"
/kranslation="PSNARY" BSGRPGLPGQQGVQGPSGPKGDKGEVGPPGPPGPPID
/translation="PSNARY" BSGRPGLPGQGFFSSSVPGPPGPPGPPID LFHLEAEMKGDKGDRGDAGQKGERGEPGAPGGFFSSSVPGPPGPPGYPGIPGPKGES
                                                                                                                                                                                                                                                                   Direct Submission
Submitted (24-NOV-1993) Marko Rehn, Department of Medical
Biochemistry, University of Oulu, Kajaanintie 52 A Fin-90220, Oulu,
Finland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA library by M. Rehn'
                                                                                                    the
                    Rehn, M., Hintikka, E. and Pihlajaniemi, T. Primary structure of the alpha 1 chain of mouse type XVIII collagen, partial structure of the corresponding gene, and comparison of the alpha 1(XVIII) chain with its homologue, alpha 1(XV) collagen chain J. Biol. Chem. 269 (19), 13929-13935 (1994)
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Matches:
Conservative:
Mismatches:
Indels:
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/clone lib="Mouse adult liver
/dev_stage="adult, 9-10 weeks"
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/citation=[2]
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/sex="male"
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    1. .1615
    /organism="Mus mus/mol_type="mRNA"
    /strain="BALB/c"

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/citation=[2]
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/citation=[2]
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80.09%
79.38%
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Rehn, M.V.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1378 CCCTGGCGGGCAGATGACATCCTGGCCAGCCCCCTGGGCTGCCCGAGCCCCCAAC 1437
                                                                                                                                                                                                                                                                                                    CCCGGAGCCCGCACCACAGCTCCTACGTGCACTGCGGCCCGGCACGACCCACAAGCCCA 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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            15
23
14
       Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                    1906 TGTGAGACGTGGCGGACGGAGGCTCCCTCGGCCACGGGCCAGGCCTCCTCGCTGCTGGGG 1965
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Human collagen type XVIII alpha 1 (COL18A1) mRNA, partial cds.
L22548
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                 161 ProArgLysSerValTrpHisGlySerAspProSerGlyArgArgLeuThrAspSerTyr 180
                                                                                CysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAla 200
                                                                                                                                                201 GlyArgLeuLeuGluGlnGluAlaAlaSerCysArgHisAlaPheValValLeuCysIle 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen
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1 (bases 1 to 3394)
Oh,S.P., Warman,M.L., Seldin,M.F., Cheng,S.D., Kholl,J.H.,
Timmons,S. and Olsen,B.R.
Cloning of cDNA and genomic DNA encoding human type XVIII collagen and localization of the alpha I(XVIII) collagen gene to mouse Genomics 10 and human chromosome 21
Genomics 19 (3), 494-499 (1994)
                                                                                                                                                                 source text: Homo sapiens cDNA to mRNA.
Location/Qualifiers
1. .3394
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185
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'db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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1. .3394
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/gene="COL18A1"
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Pred. No.:
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ACCESSION
VERSION
KEYWORDS
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HUMCOL18AX
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AUTHORS
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                                                                                PAT 07-0CT-1997
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181 CysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAla 200
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                              Unclassified.

1 (bases 1 to 3394)
Olsen, B.R. and Oh, S.P.
Collagen and uses therefor
Patent: US 5643783.A 4 01-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516
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Sequence 4 from patent US 5643783.
IS1045
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1130 c 1080 g
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1003.00
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cal Similarity:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/note=="XNBL/GenBank Accession No. L22548"
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Homo sapiens type XVIII collagen (COL18A1) mRNA, alternatively spliced, long form, complete cds.
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Saarela,J., Ylikarppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T. Complete primary structure of two variant forms of human type XVIII collagen and tissue-specific differences in the expression of the
                                                                    | codon start=1 | collagen" | codon start=1 | collagen" | product=type XVIII collagen" | product=type XVIII collagen" | collagen" | collagen | 
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LPAFVGQWTHLALSVAGGFVALYVDČEBFQRMPLARSSRGLELEPGAGLFVAQAGGAD
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RGPPGPQGPPGPPGPSFRHDKLTF1DMEGSGFGGDLEALRGPRGFPGPPGPPGVPGLP
GEPGRFGVNSSDVPGPAGLPGVPGREGPPGFPGFPGFPGPPGREGPPGRTGQKGSLGE
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                          LysProGlyAlaArgIlePheSerPheAspGlyArgAspValLeuGlnHisProAlaTrp 160
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Saarela,J., Ylikarppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T.
Direct Submission
Submitted (28-Jul-1997) Dept. of Medical Biochemistry, University of Oulu, Kajanintie 52 A, Oulu 90220, Finland
Location/Qualifiers
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/mol_type="mRNA"
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EGPGVLFAITDSAQAMVLLGVKLSGVQDGHQDISLLYTEPGAGQTHTAASFRLPAFVG
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AYIVLCIENSFWTASK"
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                                                                                                                                 'note="alternatively spliced; short form (NC1-303)"
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Matches:
Conservative:
Mismatches:
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/product="tcype XVIII collagen"
/protein_id="AAC39659.1"
/db_xref="G1:2920537"
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                          gene="COL18A1"
                                                                                                  /qene="COL18A1"
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DB:
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COMMENT

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AF018082 5408 bp mRNA linear PRI 18-MAR-1998 Homo sapiens type XVIII collagen (COL18A1) mRNA, alternatively spliced, short form, complete cds.
AF018082.1 GI:2920536
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1 (Dases I to 5408)
Saarela,J., Ylikarppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T. Complete primary structure of two variant forms of human type XVIII collagen and tissue-specific differences in the expression of the
-----GCCCACAGCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCG 1943
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Saarela,J., Ylikarppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T.
Direct Submission
Submitted (28-JUL-1997) Dept. of Medical Biochemistry, University of Oulu, Kajaanintie 52 A, Oulu 90220, Finland
Location/Qualifiers
1...5408
                                                                                                                                                                                                                                                                                                          101 GlnAspLeuTyrSerIleValArgArgAlaAspArgThrGlyValProValValAsnLeu 120
                                                                                                                                                                                                                                                                                                                                                                                                                   201 GlyArgLeuLeuGluGlnGluAlaAlaSerCysArgHisAlaPheValValLeuCysIle
                                                                                                                                        LeuAsnSerProGlnProGlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPhe
                                                                                                                                                               GlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeu
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                                                           ProValHisThrHisThrHisThrHisGlnAspPheGlnLeuValLeuHisLeuValAla
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Matrix Biol. 16 (6), 319-328 (1998)
98164096
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/mol_type="mRNA"
/db_xref="taxon:9606"
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing waryland;
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Gun,X., Gupta,J., Haghyghi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Peargon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQPPVVQLHDSNPYPRREHPHPTARPWRADDILASPPRLPEPQPYPGAPHHSSYVHLR
PRPPSPPRHSHRDFQPVLHVVALDSPLSGGMRGTRGADFQCFQQARAVCLAGFRAF
LSSRLQDLYSIVRADDRAAVPIVNLKDELLPSWEALFSGSEGPLKPGARIFSPDGKD
VLRHPTWPQKSVWHGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGQSAASC
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LWATRQAMLGQVHEVPEGWL I FVAEQEEL YVRVQNGFRKVQLEARTPLPRGTDNEVAA
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                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4425380"
/tissue type="Kidney, hypernephroma"
/clone_Tib="NIH MGC_89"
/lab_host="DH10E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
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Matches:
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Query Match:

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Score:

BASE COUNT ORIGIN

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LOCUS

RESULT 3 AK098216

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

120

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2637 bp mRNA linear PRI 08-JUL-2002
Homo sapiens, Similar to collagen, type XVIII, alpha 1, clone
BC033715
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2637)
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                                                                                                                              1016 TGTGAGACGTGGCGGACGAGGCTCCCTCGGCCACGGCCAGGCCTCCTCGCTGGGG
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                                                                                                      ProTrpArgAlaAspAspIleLeuAlaGlyProProArgLeuLeuAspProGlnProTyr
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    Indels:
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                                                                  (1-2364)
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    82.24%
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BC033715
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Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamateari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI 15-JUL-2002
highly similar
                                                             ProArgLysSerValTrpHisGlySerAspProSerGlyArgLeuThrAspSerTyr 180
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                                                                                       739 TGTGAGACGTGGCGGACGGAGGCTCCCTCGGCCAGGGCCAGGCCTCCTCGCTGCTGGGG 798
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Catarrhini, Hominidae, Homo.
CysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA linear
clone UTERU2002964,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to Homo sapiens type XVIII collagen (COL18A1) mRNA
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| organism="Homo sapiens"

| mol_type="mRNA"

| db_xref="taxon:9606"

| clone="UTBRU2009964"

| tissue_type="uterus"

| clone lib="UTBRU2"

| note="cloning vector: pME185FL3"

| 768 c 776 g 400 t
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AK098216.1 GI:21758185
Oligo capping, fis (full insert sequence)
Homo sapiens (human)
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Matches:
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Homo sapiens cDNA FLJ40897 fis,
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gai, T. and Yamamoto, J.
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source

FEATURES

BASE COUNT

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Pred. No.:

Alignment

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                                                                                                                                                                                                                                                                                 Chapman, P.W., de Luca, G. and Falciola, L. Method of producing functional protein domains Patent: WO 0210372-A 12 07-FEB-2002; Applied Research Systems ARS Holding S.A. (AN) Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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/mol_type="genomic DNA"
/db_xef="teaxon:32630"
/note="mRNA for migSP fused to (pEnd-HR#1"
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                                                                       221 GluAsnSerValMetThrSerPheSerLys 230
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Sequence 12 from Patent W00210372.
AX370851 GI:19168980
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Canis.
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                                                                                                                                                        Sheppard, M.G. and Tong, X. Methods and treating disorders
                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
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Matches:
Conservative:
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                 DNA
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/mol_type="genomic DNA"
/db_xref="taxon:9615"
1 314 c 278 g 113 t
                                                                                                                                                                                involving angiogenesis
Patent: EP 1191036-A 1 27-MAR-2002;
Pfizer Products Inc. (US)
Location/Qualifiers
1. 829
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              AX399629 829 bp
Sequence 1 from Patent EP1191036.
AX399629
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                                                        AX399629.1 GI:21335409
                                                                                   Canis familiaris (dog)
Canis familiaris
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                          OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                   2888711 seqs, 20454813386 residues
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Maximum Match 100%
Listing first 45 summaries
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), Fgapext
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AX399631 Sequence
AR183710 Sequence
AR183520 Sequence
AR217279 Sequence
AR282751 Sequence
AX490666 Sequence
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AX490666 Sequence
AX100086 Sequence
AX100086 Sequence
AX13315 Sequence
AX134075 Sequence
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AX473835 Sequence
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AX409531 Sequence
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1520548 Human colla
103714 Mus musculu
17546 Mus musculu
151044 Sequence 1
1525545 Mouse alpha
AX399631 Sequence

BC033715 Homo sapi AF018082 Homo sapi AF018081 Homo sapi

AX399629 Sequence AX370851 Sequence AK098216 Homo sapi

Description

ALIGNMENTS

AJ236873 Rattus no AB047066 Xenopus 1 AY052763 Xenopus 1

Db 82 CATACTTCCTGTATAGTTCACGTTTCATGTAATCCTCAAGAATAAAGGAAGCCAAAG 23
Qy 828 AG 829
Db 22 AG 21

Search completed: August 17, 2003, 16:22:56 Job time : 2424.32 secs

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/dev stage="fetal" |
// lab_host="DH10B" (Life Technologies) (T1 phage resistant) |
// clone llb="Ull-B-B01" |
// clone llb="Ull-B-B01" |
// note="Organ: e9e; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site-1: EcoR I; Site-2: Not I; Ull-B-B01 is a normalized cDNA library confaining the following tissue(s): fetal e9e; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oilgo-dr primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oilgonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT7T3-ECCTATACC: This library was created for the program, Gene Discovery in the Visual System, supported by National Eye magnitude (NEI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   769 GACGCTTGCCTGCACCG-TCACGTTTAATGTAATCCTCAAGAAATAAAAGGAAGCCAAAG 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 GACGGAGGCTCCCTCGGCCACGGCCCAGGCCTCCTCGCTGCTGGGGGGGCAGGCTCCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 GACTGCCTCCAAGTAGCCACCGCCTGGATGCAGATGGCCGGAGAGAGCGGCGGCGGCTCGGA
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                   /clone="UI-E-BO1-ajd-g-02-0-UI"
/tissue_type="fetal eye"
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TAG_TISSUE=human fetal eye
TAG_SEO=CGCGTATACC"

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Best Local Similarity 76.9%;
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Condinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9250
Fax: 319 335 9565
Email: bento-soares@ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
Tissue Procurement: Dr. Gregg Hageman
TONA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ thases 1 to 683)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                             CTGAAGCCCGGGGCACGCATCTTCTTTGACGCCAAGGACGTCCTGAGGCACCCCCACC
                                                                                                                           TGGCCCCCAGAAGAGCGTGTGGCATGGCTCGGACCCCAACGGGGGCGCAGGCTGACGAGGGC
                                                                                                                                                                                                                     219 ATTGAGAACAGCTTCATGACTGCCTCCAAGTAGCCACCGCCTGGATGCGGATGGCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 CCCCAGGACCTGCCTGTATTCCTGTATAGTTCACGTTTCATGTAATCCTCAAGAA
CTGAAGCCCGGGGCCCGCATCTTCTTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCC
                                                                                              TGGCCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGGCGCCCCCTGACCGACAGC
                                                                                                                                                                                            TACTGCGAGACGTGGCGGACGGAGGCCCCGGCCGACCCGGGCCAGGCGTCGTCGCTGCTG
                                                                                                                                                                                                                                                                                                                                    279 GGGGGCAGGCTCTTGGGGCAGAGTGCCGCGAGATGCCATCACGCCTACATCGTGCTCTGC
                                                                                                                                                                                                                                                                                                                                                                                   ----GGGCCTGGCCGGGACGCTTGCCTGCACG-TCACGTTTAATGTAATCCTCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM683067 693 bp mRNA linear EST 27-
UI-E-EO1-ajd-g-02-0-UI.sl UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-ajd-g-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: 1-44, >POLY A#Simple_repeat (matched compliment) Seq prime: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGAGGGGCGCCCGCAGGAGCATCCGCCGCCCCGGGG-----
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/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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DEFINITION
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AUTHORS
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623 314

254

374

503 434 443

563

494

383

554

323 614 263 674 203 734 143 768

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/dev stage="Addilt"
/lab_host="DH10B (Life Technologies)"
/clone_lib="MCI_CGAP_ENL 2"
/clone_lib="MCI_CGAP_ENL 2"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
NCI_CGAP_ENL_2 is a cDNA_library containing the following tissue(s): Enchondroma cell line (2 cell lines). The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand CDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this land and the form in this partic, of Towns
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@diowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-44, PPOLY ##Simple_repeat (matched compliment)
Seg primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCAAGGACGAGCTGTTTTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCAGGACCTCTACAGCATCGTGCGCCGCCGCACCGCCACCGGGGTGCCCGTCGTCAAC 357
                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAGGGACGAGGTGCTCTTCCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCCAG
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TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
                                                                              Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 703)
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47.6%; Score 394.4; DB 13; Length 703;
Best Local Similarity 76.6%; Pred. No. 6.6e-66;
Matches 520; Conservative 0; Mismatches 132; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   James Martin from University of Iowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="U1-H-FGO-bcp-p-10-0-UI"
/tissue_type="Enchondroma cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 t
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224 c 228 g
                                           sapiens (human)
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UI-H-FG0-bcp-p-10-0-UI.s1 NCI CGAP_EN1_2 Homo sapiens cDNA clone
UI-H-FG0-bcp-p-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                            /note="Organ: ovary;" Vector: pOTB7; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGCTCCCTCGGCCACGGGCCAGGCCTCCTCGCTGCTGGGGGCAGGCTCCTGGGGCA 233
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                                                                                                                                                                                                                                                                                                                                                                           GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using SAP-CNNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTGCGCGTGCCGACCGCGCACGTGCCCATCGTCAACCTCAAGGACGAGGTGCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 944;
                                                                                                                      /tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 398.2; DB 13; Length
Pred. No. 1.2e-66;
0; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                   /clone="IMAGE:6650260"
    /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                        297 GCCAGGCCTCCTCGCTGCTGGCGGGCCGGCTGCTGGAGCAGAAGCCGCCGGGTGCCACA
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Email: cgapbs-remail.nih.gov
Trissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2895 row: d column: 04
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                                                                218 GGGGAGCGGACTTCCAGTGCTTCCAGCAGGCGCGCCGCCGGGGGCTGGCCGGCACCTTCC
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AGENCOURT 10434549 NIH MGC_109 Homo sapiens cDNA clone IMAGE:6650260 5', mRNA sequence.
   Indels
         Mismatches 105;
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/organism="Homo sapiens"
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Location/Qualifiers
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         464; Conservative
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BU859398/c
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1. (bases 1 to-657)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.B. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 25-MAR-2003
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/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled From multiple tissues
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217 c 219 g 113 t 1 others
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CB444165
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/organism="Bos taurus"
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/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
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RESULT 12 CB444165/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS BASE COUNT ORIGIN

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                               VERSION
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AUTHORS
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                                                                                                                                                          /tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1:1 kb. Library constructed by Life
Technologies."
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0
                                                                                                                                                                                                                                                                                                                          Length 757;
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Pred. No. 2.9e-71;
0; Mismatches 136; Indels
     at:
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found through the I.M.A.G.E. Consortium/LLNL http://image.lln.gov
Plate: LLAM9709 row: i column: 09
High quality sequence stop: 757.
Location/Qualifiers
                                                                                                                                                                                                                                                                             119 t
                                                                                               /organism="Homo sapiens"
                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3904208"
                                                                                                                                                                                                                                                                           235 g
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                                                                                                                                                                                                                                                                                                                          tch 51.0%;
al Similarity 78.8%;
504; Conservative
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Best Local Similarity
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BI412588 874 bp mRNA linear EST 14-AUG-2001 602990468F1 NCI\_CGAP\_Lu33 Mus musculus cDNA clone IMAGE:5146409 5',

BI412588 LOCUS DEFINITION

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1361 row: g column: 18
High quality sequence start: 23
High quality sequence start: 23
High quality sequence stop: 808.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACACCCACACCCACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCCCTGAAC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 CTCTCACTTGCTCATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTGGCACTGAAC 190
                                                                                                             Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae; Murinae; Mus.
1 (Dases 1 to 874)
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                                                                                                                                                                                                                                                                                                                                                                                           M. Fatima
                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert, Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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/strain="CZECH II"
BI412588
BI412588,1 GI:15173511
                                                                                      Mus musculus (house
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DEMUNESS: 757 bp mRNA linear EST 20-OCT-2000 601502237F1 NIH_MGC_70 Homo sapiens CDNA clone IMAGE:3904208 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                          121 GCGGGCCGTGGGGGCTGGCGGGCCTTCCTGTCCTCTCCTGCGCCTGCAGGACCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GAGCGTGTGGCATCGGACCCCCAACGGGCGCAGGCTGACCGAGAGCTACTGTGAGAGC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GECACGCATCTTCTCCTTTGACGCCAAGGACGTCCTGAGGCACCCCACACTGGCCCCAGAA 360
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                                                                                                             129 CACCCACACCCACACCCACCAGGACTTCCAGCTGGTGCTGCACCTGGTGGCCCTGAACAG
                                                                                                                                                                                               189 CCCGCAGCCGGCCGATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTCCAGCAGGC
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCCAGCTGAAGCCCGG
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                         Length 707
                                                                  Indels
           51.0%; SCote 78.2%; Pred, No. 2.4e-,...
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Homo sapiens
                                             Best Local Similarity 78.2
Matches 508; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE908201 707 bp mRNA linear EST 20-OCT-2000 601500458F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902175 5',
                                         E 1 (Dasses 1 to 70).

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM9704 row: d column: 16

High quality sequence stop: 688.

Location/Qualifiers
CTCAACAGCCCCCTGTCAGGCGGCATGCGGGGCCATCCGCGGGGCCGACTTCCAGTGCTTC 363
                                                                                                                                 420
                                                                                                                                                                                                                                                               484 AAGGACGAGCTGCTGTTTCCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTG 543
                                                                                                                                                                                                                                                                                                          480
                                                                                                                                                                                                                                                                                                                                     544 AAGCCCGGGGCACGCATCTTCTCCTTTGACGCAAGGACGTCCTGAGGCACCCCACCTGG 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGAGACGTGGCGGACGGAGGCCCCGGCGCCACCGGGCA-GGCGTCGTCGCTGCTGGC 599
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 707)
                                                                                                                                                                                                                                                                                                          AAGCCCGGGGCCCGCATCTTCTTTTCGACGCCAGAGATGTCCTGCAGCACCCCGGCCTGG
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3902175"
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KEYWORDS
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TITLE
JOURNAL
COMMENT
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ACCESSION

REFERENCE

FEATURES

RESULT 9 BE908201

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/clone="IMAGE:6584644"
/tissue type="teratocarcinoma, cell line"
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/clone lib="NIH MGC 109"
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/note="Organ: ovary; Vector: poTB7; Site 1: EcoR1; Site 2:
/note="Organ: ovary; Vector: poTB7; Site 1: EcoR1; Site 2:
/note="Organ: ovary; Vector: poTB7; Site 1: EcoR1; Site 2:
/note="Organ: ovary; Vector: priming bit ovary; Vector ovary; V
                                                                                                                                                                                                                                             BUSS6872 947 bp mRNA linear EST 16-SEP-2002 AGENCOURT 10186760 NIH MGC_109 Homo sapiens cDNA clone IMAGE:6584644 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
CCCTGGCGGGCAGATGACATCCTGGCCGGCCCCCCCGCGCCTGCTGGACCCCCAGCCCTAC
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Argaed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2795 row: f column: 04
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Pred. No. 6.3e-72;
0; Mismatches 82
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               616.
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Location/Qualifiers
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Best Local Similarity 84.2%;
Matches 508; Conservative (
                                                                                  615
                                                                                                                                 687 GGCAAGCTTCTTGGG 701
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Homo sapiens
                                                                                  601 GGCAGGCTGCTGGAG
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/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
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                                                                               HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------CCCACCGCCCACAGCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCG
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Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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                                                                                                                                                                                                                                                                   1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/cell_type="textocarcinoma"
/cell_line="NT2"
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                                                                                                                                                                                     Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
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Matches 506; Conservative
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/note="Organ: liver, Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                           CCCGGGG----CCCCGCACCACGGCTCCTACGTGCACTTCCAGCCGGCTCGCCCCACTGGT
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Pred. No. 2.4e-72;
0; Mismatches 140;
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| 547; Conservative
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                                                                  CAGCAGGCGCGCGCGGGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGCTG 300
                                                                                    CAGGACCTCTACAGCATCGTGCGCCGCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTC 360
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LinL at:

http://image.lln.gov
Plate: LiLAM9531 row: i column: 05

High quality sequence stop: 761.
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NHH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                   ACTGCGAGACGTGGCGGACGGACGGACGGCCCCGGCGACGGCGAGGCGTCGCTGGTGG
 CTGAACAGCCCGCAGCCGGCGCGCATGCGAGGCATCCGGGGAGCGGACTTCCAGTGCTTC
                                                                                                                                                                                                                               AAGGACGAGCTGCTGTTTCCCAGCTGGAGGCTCTGTTCTCAGGCTCTGAGGGTCGGCTG
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/clone="INAGE:4195660"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
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Mus musculus
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/strain="FVB/N"
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/ organism="Bos taurus"

/ organism="Bos taurus"

/ db xref="taxon:9913"

/ tissue_type="pooled"

/ tissue_type="pooled"

/ lab hoste:"bh108"

/ clone_lib="Wector: pcMV SPORT6; Site_1: NotI; Site_2: SalI; ...

Library made from pooled tissue from testis, thymus, semitendonesus muscle, longissimus muscle, pancreas, adrenal, and endometrium:

30 a 200 c 179 g 92 t
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Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 623)
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                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.C. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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PO Box 166, Clay Center, NE 68933-0166, USA
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                   Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 81 row: F column: 9
Seq primer: ATTTAGGTGACACTATAG.
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43.00
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Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                      Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washingron University Genome Center. Vector Trimmi g: Cross match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 25-APR-2001
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinae; Bos.
1 (bases 1 to 551)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="Dilib"
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/clone_lib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pT/713Pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laborators and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
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                                                  H
    W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221883 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BF074459
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Matches:
Conservative:
Mismatches:
Indels:
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BACKWARD: ATTAAACCTCACTAAAG
INSET Length: 279 Std Error: 0.00
Plate: BP230015B10 row: C column: 11
Seg primer: AGGGAATAACAATTTCACACAGGA
High quality sequence stop: 279.
Location/Qualifiers
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/organism="Bos taurus"
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                                                                                           Tel: 217 333 5998
Fax: 217 244 5817
Email: h-lewin@uiuc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female
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Bos taurus
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Best Local Similarity:
                                                                        61801, USA
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Query Match:
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DEFINITION
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BF074459
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TITLE JOURNAL

COMMENT

AUTHORS

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Fmail: waith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: FQY8051 row: I column: 11
Seq primer: TAGAAGGCACAGTCGAGG.
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Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990319.
Plate: FQY8051 row: I column: 11
Seq primer: GTAATACGACTCACTATAGGG.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                             1. 657
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                             Location/Qualifiers
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Query Match:
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AUTHORS
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CB443805
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Plate: FQY8006 row: I column: 12
Seq primer: TAGAAGGCACAGTCGAGG.
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1 (bases 1 to 657)

Smith T. P.L., Roberts A. J., Echternkamp, S.E., Chitko-McKown, C.G., Waray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mostarian-mena.
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/db Arref="mana."
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/lab Anost="DB10B"
/clone lib="Manac Bobu"
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placenta/endometrium.
placenta/endometrium.
placenta/endometrium.
placenta/endometrium.
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                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
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USDA, ARS, US Meat Animal Research Center
PD Dox 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
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Matches:
Conservative:
Mismatches:
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CB444165.1 GI:29233914
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Query Match

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Score:

BASE COUNT

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DEFINITION ACCESSION

ORGANISM

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REFERENCE AUTHORS

TITLE JOURNAL COMMENT

CB444165/c LOCUS

RESULT

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location/Qualifiers
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1 (bases I to 387)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                           618
                                                                                                                                                                                                                                                                                                                                                                                                    83
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                                                  ArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAlaGlyLeuAla
                                                                                                                                                                                                                                                                                                                                                                         BF601253 387 bp mRNA linear 266182 MARC 3BOV BOS taurus CDNA 5', mRNA sequence.
                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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              organism="Bos taurus"
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BACKWARD: GTTTCCCAGTCACGACG
Plate: 40 row: H column: 7
Seg primer: ATTTAGGTGACACTATAG.
                            /mol_type="mRNA"
/db_xref="taxon:9913"
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PCR PRimers
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Fax: 402 762 4390
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483 bp mRNA linear EST 22-MAY-2001 G02726433F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4865936 5', BG823096
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/mol type="mRNA"
/db Xref="taxon:9606"
/clone="IMAGE:14665936"
/tissue_type="adenocarcinoma cell line"
/lab_host="DHIOB (phage-resistant)"
/clone_lib="NHH MGC_15"
/note="Organ: colon; Vector: pOTB7; Site_1: Xhol; Site_2:
Colone lib="NHH MGC 15"
/note="Organ: colon; Vector sites using the following 5;
adaptor: GGCACGAG(G). Size-selected >500bp for average
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4813)
11 H-WGC http://mgc.noi.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CTGTCCTCGCGGTTGCAGGACCTGTACAGCATCGTGCGCCGCCGCCGACCGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 LeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArgAlaAspArg 112
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 479.
Location/Qualifiers
                                       /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-938-391-2 (1-230) x BF601253 (1-387)
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/organism="Bos
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Alignment Scores:
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Jab host="E. coli EMOH10B"
/clone lib="Normalized Reset Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"
/note="Vector: pCMVSPORT6; Library made from equivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pgm_l.pk006.hl7 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library (pgm2n.pk006.hl7 S. similar to gb AAC31294.2 (AF083440) collagen XVIII [Gallus gallus], mRNA sequence.
BM488074. GI:18609005
                                                                                                                                                                                                                                                                                                                                                               270 GGCGGCATGCGGGGCATCCGCGGGGCCGACTTCCAGTGCTTCCAGCAGGCGCGGGCCGCT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthemis kit (Stratagene) and Superscript II RT (Life Technologies)" 200 c 146 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:9031"
/clone="pgm2n.pk006.h17".
/sex="wale and Female"
/tissue type="Breast muscle, leg muscle and epiphyseal
growth plate"
                                                                                                                                                                                                                                                                                               GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 577)
Cogburni.A. and Monsonego-Ornan, E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cogburn@udel.edu, www.chickest.udel.edu
                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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/strain="Commercial broiler and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Gallus gallus"
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/dev stage="adult"
//dev stage="adult"
//lab_host="phi0B"
//clone_lib="CSEQRBN19"
//clone_lib="CSEQRBN19"
//note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Notl; This normalized library was
constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with ECORI
, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU459935 614 bp mRNA linear EST 29-NOV-2002 603367327F1 CSEQRBN19 Gallus gallus cDNA clone ChEST268f8 5', mRNA
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Gallus gallus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Phasianinae; Gallus.

1 (Basea I to 614)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 GGGCTGGCCGGTACCTTCCTTCCTCCTCCCGCCTGCAGGACCTGTACAGCATC 318
                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                      9 others
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Conservative:
Mismatches:
Indels:
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Fax: 01612360409
Email: Simon Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
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/clone="ChEST268f8"
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BU459935
BU459935.1 GI:25949246
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1 (bases 1 to 652)

Boardman, P.E., Sana-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Not1 adapters, digested with EcoRI
pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1966): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BUJ52506 <sup>2</sup> 652 bp mRNA linear EST 28-NOV-2002
603527982F1 CSEQCHN69 Gallus gallus cDNA clone ChEST477d22 5', mRNA
sequence.
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University of Manchester Institute of
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/mol_type="mRNA"
/strain="Compton line 151"
/db_xref="taxon:9031"
/clone="ChEST477d22"
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Matches:
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/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Simon. Hubbard@umist.ac.uk.
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Gallus gallus
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Fax: 01612360409
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BU352506
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, size-selected, and cloned into the Not1 and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridiation was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 20-MAY-2003 ary (pgm2n)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler chickens, Ottawa Research Ctr
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'clone lib="Normalized chicken muscle cDNA library (pgm2n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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growth plate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD215096 678 bp mRNA linear EST 20-MA) pgm20.pkm20.pkm30.pkm20.pkm21.cd dhicken muscle cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk013.n20 5' similar to gb|AAC33294.2 (AF083440) collagen XVIII [Gallus gallus], mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.chickest.udel.edu.
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Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest
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Cogburn, L.A. and Monsonego-Ornan, E.
Chicken ESTs from muscle
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/clone="pgm2n.pk013.n20"
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CD215096.1 GI:30954764
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1 (bases 1 to 706)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                              87 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 106
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mol type="mRNA"

strain="Layer and broiler"
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Fax: 01612360409
Email: Simon. Hubbard@umist.ac.uk.
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/clone="ChEST183g14"
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BU439577.1 GI:25928888
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Gallus gallus
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(basianinae; Gallus.

(basianinae; Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J. A Comprehensive Collection of Chicken cDNAs

(curr. Biol. 12 (22), 1965-1969 (2002)
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604164521F1 CSEQCHN55 Gallus gallus cDNA clone ChEST1021j6 5', mRNA
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University of Manchester Institute of Science and Technology (UMIST
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/mol_type="mRNA"
/strain="Compton Line 151"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

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US-09-938-391-2 (1-230) x BU439577 (1-706)

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Search completed: August 18, 2003, 03:41:27<sup>-</sup> Job time: 2045.89 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Total number of hits satisfying chosen parameters:

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GenEmbl:* : gb_ba: <u>*</u> : gb_htg:* : gb_in:* : gb_om:*	gb_ro:* gb_sts:* gb_sy:* gb_un:*	gb_vi:* em_ba:* em_fun:* em_hum:*	em_in:* em_mu:* em_om:* em_or:*		em_sts:* em_un:* em_vi:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleos! Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis. REFERENCE AUTHORS TITLE

1 Sheppard,M.G. and Tong,X. Methods and compositions for diagnosing and treating disorders involving angiogenesis

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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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Methods and compositions for diagnosing and treating disorders involving angiogenesis
Patent: EP 191036-A 1 27-MAR-2002;
Pfizer Products Inc. (US)
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/db_xref="taxon:9615"
1 203 c 191 g 83 t
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EP 1191036-A 3 27-MAR-2002;
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        Pfizer Products Inc. (US)
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O'Reilly,M.S. and Folkman,M.Judah.
Therapeutic antiangiogenic endostatin compositions
Patent: US 6346510-A 6 12-FEB-2002;
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/organism="Canis familiaris"
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Sequence 6 from patent US 6346510.
AR193166 GI:20239131
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175 g
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Best Local Similarity 100.
Matches 555, Conservative
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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BASE COUNT ORIGIN

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                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Angiostatin and endostatin binding proteins and methods of use
Patent: WO 0193897-A 30 13-DEC-2001;
EntreMed, Inc. (US)
Location/Qualifiers
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4.7%; Score 26; DB 6; Length 552;
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            Sequence 4 from Patent WO0119989.
AX100086
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196 c 179 g 9
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Sequence 2 from Patent WO0230982.
AX473835 AX473835.1 GI:22208005
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Boerner, R.J., Bermejo, L.L., Mistry, F.R., Shepard, S.R. and
Schrimsher, J.L.
                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Patent: WO 0119989-A 10 22-MAR-2001;
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Pred. No. 0.13;
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O'Reilly,M.S. and Folkman,M.Judah.
Therapeutic antianglogenic endostatin compositions
Patent: US 6346510-A 4 12-FEB-2002;
Location/Qualifiers
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ive 0; Mismatches
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Sequence 10 from Patent W00119989.
AX100092 AX100092.1 GI:13539063
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Sequence 4 from patent US 6346510.
AR193165 GI:20239130
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
189 c 176 g ?
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                                                                 EntreMed, Inc. (US)
Location/Qualifiers
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196 c 177 g
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TITLE JOURNAL FEATURES

AUTHORS REFERENCE

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Gaps

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/product="type XVIII collagen"
/product="type XVIII collagen"
/product="type XVIII collagen"
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GTFRAFLSSRLDGDLYSIVRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIF
SFNGKDVLTHPTWPQKSVWHGSDPWGRRLTESYCETWRTEAPSATGQAYSLLGGRLLG
QSAASCHHAYIVLCIENSFWTASK"

a 196 c 177 g 95 t
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Zhi Yong H., Biao, L., Wei-Jie, Z. and Xiang-Fu, W.
Direct Submission
Submitted (07-SEP-1999) Shanghai Institute of Biochemistry, Chinese Academy of Sciences, 320 Yueyang Road, Shanghai 200031, P. R. China Location/Qualifiers
                                                                                                                                                                                               PRI 06-OCT-1999
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Cloning and expression of human endostatin gene in Escherichia coli
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Feng, Y., Cui, L. B., Liu, C. X. and Ma, Q. J.
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Sheng Wu Gong Cheng Xue Bao 17 (3), 278-282 (2001)
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--ive 0; Mismatches
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1. .555
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/organism="Homo sapiens"
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Fused proffein containing angiostatin component and utilization
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I (basea I to 552)

Bolanowski, M.A., Caparon, M.H., Casperson, G.F., Gregory, S.A., Klein, B.K. and Mckearn, J.P.

Klein, B.K. and ontaining angiostatin component and utilization patent: JP 2001s18304-A 50 i6-OcT-2001;

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GD Homo sapiens (human)

PN JP 2001s18304-A/50

PD 16-OCT-2001
                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MARK A BOLANOWSKI, MAIRE H CAPARON, GERALD F CASPERSON, SUSAN A
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C12N15/09, A61K38/00, A61K48/00, A61P9/10, A61P35/00, C07K14/52,
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                                                                                                                Sim, K.L. and Liang, H.
Angiogenesis-inhibiting peptides and proteins and methods of Patent: WO 0230982-A 2 18-APR-2002;
EntreMed, Inc. (US)
Location/Qualifiers
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Location/Qualifiers
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Homo sapiens multi-functional protein MFP mRNA, complete cds.
AF282883
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GTGADPQCFQQARAVGLAGFFRAFLSSRLQDLYSIVRRADBAAVPIVNLKDELLFPS
WEALFSGSEGPLKFGARIFFSFDGKDVLRHFYWPQKSVWHGSDPNGRRLTESYCETWRT
EAPSATGQASSLLGGRLLGGSAASCHHAYIVLCIENSFWTASK"
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                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (27-JUN-2000) R & D, Robinson Biotech Corp., 24634 Five Mile Road, Suite 24-26, Redford, MI 48239, USA
Location/Qualifiers
1. .786
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 786)
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/db_xref="GI:21425751"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chapman, P.W., de Luca, G. and Falciola, L. Method of producting functional protein domains Patent: WO 02103724 12 07-FEB-2002; Applied Research Systems ARS Holding S.A. (AN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26; DB 9;
Pred. No. 0.13;
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/note="antiangiogenic agent"
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AX370851
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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178 GACTTCCAGTGCTTCCAGCAGGCGCG 203
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                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
1. 786
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100.0%; Pre
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a 336 c
                                                                                                                                                                                         Homo sapiens (human)
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DEFINITION
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AUTHORS
TITLE
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ORIGIN
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AUTHORS
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VERSION
KEYWORDS
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VERSION
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SOURCE
                                                       RESULT 13
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/db_xref="GI:17226298"
/trānslation="SPPAHSHRDFQPVLHLVALNSPLSGGMRGIRGADFQCFQQARAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLAGTFRAFLSSRLQDLYSIVRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGA
RIFSFDGKDVLRHPTWPQKSVWHGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGR
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                                                                                                                                                                                                                                                                                                                         <1. .564
/note="similar to endostatin; can inhibit endothelial cell
                                                                                                                                                                       Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="synthetic construct"
/mol_type="genomic DNA"
/mol_txpe="senon:0350"
/db xrefe="taxon:39-41 for /noce="mRNA for mIgSP fused to COL18A1 exons 39-41 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                   Feng,Y., Wu,Y., Zhu,X., Liu,C.X. and Ma,Q.J.
Endostatin contributes to maintain cartilage homeostasis via
promotion of the anabolic program of chondrocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                       Unpublished

(Leases 1 to 564)

Peng, Y., Cui, L.B. and Ma, Q.J.

Direct Submission

Submitted (03-SEP-2001) Genetic Engineering, Beijing Ins

Biotechnology, Taiping Road, Beijing 100850, P.R. China

Location/Qualifiers
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4.7%; Score 26; DB 6; Length 650;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 564;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <1. .561
/note="Region: NC1 domain"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                      'product="collagen XVIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14 from Patent WO0210372.
AX370853
                                                                                                                                                                                                                             1. .564
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 g
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synthetic construct
artificial sequences.
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                   (bases 1 to 564)
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RESULT 12 AX370853 LOCUS ORGANISM

REFERENCE AUTHORS JOURNAL

FEATURES

VERSION KEYWORDS SOURCE ACCESSION

BASE COUNT ORIGIN

BASE COUNT ORIGIN

; 0

Gaps

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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (G-JUL-2002) Tel:81-438-52-3975, Fax:81-438-52-3986) (E-mall:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) WEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                  AKO98216
2364 bp mRNA linear PRI 15-JUL-2002 Homo sapiens cDNA FLJ40897 fis, clone UTERU2002964, highly similar to Homo sapiens type XVIII collagen (CCL18A1) mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                               Gaps
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                            0; Indels
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/tissue type="uterus"
/clone lib="UTERU2"
/note="cloning vector: pME188FL3"
776 g 400 t
                                                                                                                                                                                                                                                                                                                                                                                                        oligo capping; fis (full insert sequence)
Homo sapiens (human)
Best Local Similarity 100.0%; Pred. No. 0.13; Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDO human cDNA sequencing project
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/db_xref="taxon:9606"
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Isogai,T. and Yamamoto,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                           AK098216
AK098216.1 GI:21758185
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Best Local Similarity 100.
Matches 26; Conservative
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AUTHORS
TITLE
JOURNAL
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AK098216
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Search completed: August 17, 2003, 18:39:19 Job time : 2788.23 secs ö

Gaps

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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Italgudi, Raghunath V.
APPLICANT: Itol-dura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFRENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
NUMBER OF SEQ ID NOS: 7600
SEQ ID NO 2718
LENGTH: 273
TYPF: ...
TYPF: ...
                                                                                         Query Match 4.7%; Score 26; DB 1; Length 3394; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 26; Conservative 0; Mismatches 0; Indels
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CTHER INFORMATION: Incyte ID No. 6476212 700553162H1
NAME/KEY: unsure
LOCATION: 88, 189, 238, 243, 246, 255, 260
COTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-2718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: Windows 95
FastSEQ for Windows Version 2.0b
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Patent No. 6090911
GENERAL INFORMATION:
APPLICANT: Petka, Wendy A.
APPLICANT: Tirrell, David A.
APPLICANT: Kevin P. MGrath
TITLE OF INVENTION: REVERSIBLE HYDROGELS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.2%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 56; Matches 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 CGCCGCCACCGGCCAGG 445
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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STRANDEDNESS:
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TOPOLOGY: 1i
US-08-159-784-4
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                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas
APPLICANT: MacDonald, Nicholas
APPLICANT: Sim, Kim Lee
TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and
TITLE OF INVENTION: Proteins and Methods of Use
TITLE OF INVENTION: Proteins and Methods of Use
CURRENT APPLICATION NUMBER: US/09/206,059
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SEQ ID NOS: 80
SEQ ID NO 30
LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.7%; Score 26; DB 3; Length 552; 100.0%; Pred. No. 0.017; ive 0; Mismatches 0; Indels
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Patent No. 5643783
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
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REPERENCE/DOCKET NUMBER: 00246/170001
FELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 GACTTCCAGTGCTTCCAGCAGGGGGG 113
       88 GACTTCCAGTGCTTCCAGCAGGCGCG 113
                                               88 GACTTCCAGTGCTTCCAGCAGGCGCG 113
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                                                                                                                                                             ; Sequence 30, Application US/09206059
; Patent No. 6201104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-206-059-30
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 02110-2804
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                                                                                                                 RESULT 3
US-09-206-059-30
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US-08-159-784-4
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STATE:
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sequence 3, Appli Sequence 15090, A Sequence 15090, A Sequence 12345, A Sequence 9, n

5525, Ap 16122, A 12208, A 2299, Ap

Sequence Sequence Sequence

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Sequence Sequence Sequence

Sequence 16481, A Sequence 1, Appli Sequence 1, Appli Sequence 16, Appl

Sequence

OM nucleic

Run on:

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; Sequence 6, Application US/09315689
; Patent No. 6345510;
; GENERAL INFORMATION:
; APPLICANT: FOIKman, Judah
; APPLICANT: FOIKman, Judah
; TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
; FILE REFERENCE: 05213-0229
; CURRENT APPLICATION NUMBER: US/09/315,689
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 6
; SCOTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; ID NO 6
; TENAMER.
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Sequence 4, Application US/09115689

Serient No. 6346510

GENERAL INFORMATION:
APPLICANT: Polkman, Judah

APPLICANT: O'RAIlly, Michael

TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REPERENCE: 05213-0229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 4; Length 534;
Pred. No. 0.017;
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4.7%; Score 26; DB 4; Length 546;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 26; Conservative 0; Mismatches 0; Indels
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US-09-398-496-3
US-09-252-991A-15090
US-09-252-991A-12345
             US-09-252-991A-2385
US-09-252-991A-5525
US-09-252-991A-16122
US-09-252-991A-12208
US-09-252-991A-2299
US-09-252-991A-12294
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US-09-252-991A-16481
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-08-813-940-3
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100.0%; Pred. No. c...
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CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
LENGTH: 546
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ORGANISM: Homo sapiens
US-09-315-689-6
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CRGANISM: Homo sapiens
US-09-315-689-4
US-09-315-689-4
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 Query Match
Best Local S:
Matches 26
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Sequence 12, Appl
Sequence 11, Appl
Sequence 16492, A
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10, Appl
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Sequence 5585, Ap
Sequence 2533, Ap
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Sequence 16110, A
Sequence 1, Appli
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Sequence 1, Appl
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4332.442 Million cell updates/sec
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                                                                                                          August 17, 2003, 16:25:28 ; Search time 56.5426 Seconds
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US-09-206-059-4
US-09-206-059-3
US-08-159-784-4
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US-08-956-307B-10
US-08-956-307B-3
US-09-449-293-3
US-09-449-293-3
US-09-561-108-12
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US-09-252-991A-16260
US-09-252-991A-5585
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                                                                          - nucleic search, using sw model
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Specific tumour ce Reproductive recom Anticancer gene-as Synthetic plasmid DNA encoding a hum Synthetic plasmid Nucleotide sequenc DNA encoding human Human alpha-1 coll Human alpha-1 coll Gene #2178 used to

Human collagen 18 Nucleotide sequenc Human immune/haema

Human pancreatic c Human collagen XVI

Human ovarian anti

Canine endostatin Canine collagen XV Canine endostatin Canine collagen XV

Human immune/haema

Human endostatin c Human endostatin c Human pancreatic c Human endostatin e

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Human endostatin c SEQ ID 50 of WO991 Nucleotide sequenc Human endostatin c

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Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; plaque neovascularisation; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiathritic; antipsoriatic; antidiabetic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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                                                                                    August 17, 2003, 14:11:23 ; Search time 214.14 Seconds (without alignments) 6996.296 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, tellangiectasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, isohaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 555 BP; 78 A; 203 C; 191 G; 83 T; 0 other;
                                                                                                                                                                                                                                            encodes an endostatin protein -
                                                                                                                                                                                                                                                                            Claim 2; Fig 4; 56pp; English
                                                                25-AUG-2000; 2000US-227924P
                                24-AUG-2001; 2001EP-0307224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endostatin coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 555; Conservative
                                                                                              (PFIZ ) PFIZER PROD INC
                                                                                                                              Tong X;
                                                                                                                                                            WPI; 2002-354068/39.
                                                                                                                                                                             P-PSDB; AA017430
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27-MAR-2002
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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of anglogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial anglogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, anglofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, isohaemic limb anglogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; ecrebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dog, pro-endostatin, endostatin, angiogenesis, cancer, gene therapy, psoriasis, rheumatoid arthritis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated nucleic acid molecule for the treatment of angiogenesis-related disorder, such as cancers or diabetic retinopathy, encodes an endostatin protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 829 BP; 124 A; 314 C; 278 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "pro-endostatin"
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555
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                                                                      541 rccrrcrccaagrag
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Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -

98US-0097883

25-AUG-1999; 25-AUG-1998;

02-MAR-2000.

(LEXI-) LEXINGEN PHARM CORP

Gillies SD;

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2000-237616/20 P-PSDB; AAY70265

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                                                                                                             GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC 180
                                                                                                                                                        GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGCGGCCTGCAGGACCTCTACAGAGATC 318
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    GAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGTTCTGCAGAACAGCGTCATGACC 678
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                                                        139 CACACCCACCAGGACTTCCAGCTGGTGCTGCTGGTGGCCCTGAACACGCCCGCAGCCG
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/note= "Does not include stop codon"
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Mismatches
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Intinition between the management of the fusion protein (immunofusing angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including the managiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental collibroplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of angiofibroma, wound granulation, and excessive or abnormal stimulation of hypertrophic scars, i.e. kelolid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encoding canine endostatin used in the construction of immunofusin containing canine
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                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 AGCGGACTTCCAGTGCTTCCAGCAGCGCGCCGCGCGGGCTGGCCGGCACCTTCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 AGCGGACTTCCAGTGCTTCCAGCAGCGCGCCCCGCGGGGCTGGCCGGCACCTTCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 CTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATCGTGCGCCGCGCCGACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCCCGTCGTCACCTCAGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 CCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGGCACGGCTCCGACCCCAGCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCGGGCGGCATGCGAGGCATCCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACGGAGGCCCCCGGCGGCCACCGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.3%; Score 529; DB 21; Length 552; 100.0%; Pred. No. 8.1e-228; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 552 BP; 77 A; 204 C; 190 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   Example 8; Pages 58-59; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin Fc fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 529; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
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g
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443

384 CCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACGGAGGCCCCGGCGGCGCCACCGGGCA

WO200011033-A2

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Human; endothelial cell proliferation inhibitor; collagen XVIII; angiogenesis inhibitor; anti-tumour; cytostatic; antipsoriatic; vasotropic, determatological; ophthalmological; vulnerary; antiarteriosclerotic; antidiabetic; haemostatic; contraceptive; coular angiogenic disease; atherosclerosis; scleroderma; myocardial angiogenesis; telangiectasia; angiofibroma;
                       Alternate human endostatin gene sequence.
                                                                                                                                                                                                                                                                                                                              (CHIL-) CHILDRENS MEDICAL CENT.
11-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                      O'Reilly MS, Folkman MJ;
                                                                                                                  wound granulation, ds.
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-365617/31.
P-PSDB; AAY94324.
                                                                                                                                                                                                                        WO200026368-A2.
                                                                                                                                                                                                                                                                     01-NOV-1999;
                                                                                                                                                                                                                                                                                           30-OCT-1998;
                                                                                                                                                                                                                                                                                                      20-MAY-1999;
                                                                                                                                                                                                                                               11-MAY-2000
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                        The present sequence encodes human endostatin, an angiogenesis inhibitor, derived from human liver cDNA. This is the C-terminal protecolytic fragment of collagen 18a. Endostatin can inhibit endothelial cell proliferation in vitro and angiogenesis in vivo. This is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the construction of the expression plasmid for the treatment of mammalian diseases, especially cancer. The plasmids can be used for (in vivo) transfection of a cell in situ in order to medulate tumour activity. Anti-angiogenic gene inhibits growth of solid tumour and lung metastatic tumours by intravenous or intramuscular delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmids comprising tissue specific transcription elements linked to a
anti-angiogenic gene is useful transfection of cells and treatment of,
                                                                                                                                                                                                                                   Human endostatin; angiogenesis; expression plasmid; tumour activity;
cancer; anti-angiogenic agent; solid tumour; lung metastatic tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                     CTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACTCCTTCTCCCAAG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.2%; Score 29; DB 21; Length 552; 00.0%; Pred. No. 0.0026; Ve 0; Mismatches 0; Indels
                                                        CTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACCTCCTTCTCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                          Sullivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 552 BP; 87 A; 223 C; 173 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          Ralston R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCTGCACCTGGTGGCCCTGAACAGCCC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 GIGCIGCACCIGGIGGCCCIGAACAGCCC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 40, 103pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Mehrens D,
                                                                                                                                       AAZ50398 standard; cDNA; 552
                                                                                                                                                                                                                                                          cytostatic; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                      99WO-US16388.
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                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29; Conservative
                                                                                                                                                                                                             Human endostatin cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                         Szymanski P,
                                                                                                                                                                                                                                                                                                                                                                                                   (VALE-) VALENTIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-183133/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                       WO200006759-A2.
                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                      18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                      20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                             27-JUL-1998;
                                                                                                                                                                                                                                                                                                                              10-FEB-2000.
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                                444
                                                        504
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                                                                                                                                                              AAZ50398;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Min W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
AAA27005
ID AAA2
XX
AC AAA2
                                                                                                                 RESULT 4
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/product= "Endostatin protein"

98US-0106343. 99US-0315689.

99WO-US25605

Location/Qualifiers

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protein. When the human endostatin gene sequence AAA27004 is
recombinantly expressed, an observable doublet of protein results, both
versions of which are functional endostatin proteins. The present gene
sequence encodes an endostatin variant which is the same as the protein
encoded by AAA27004 minus the first four amino acids. Recombinant mouse
encoded by AAA27004 minus the first four amino acids. Recombinant mouse
encoded by AAA27004 minus the first four amino acids. Recombinant mouse
encoded by AAA27004 minus the first four amino acids. Recombinant mouse
confortatin (20 mg/kg) was administered subcutanceusly to mice implanted
with Lewis lung carcinomas. There was tumour mass regression
non-detectable levels after 12 days of therapy due to the angiogenesis
inhibitory activity of endostatin. Thus the protein is useful for
treatment of angiogenesis dependent cancers. The polymucleotide and
colypeptide sequences of this endostatin are useful for treating and
diagnosts of tumours, ocular angiogenic diseases, Osher-Webber syndrome,
myocardial angiogenesis, plaque neovascularisation, telangiectasia,
chaemophiliac joints, angiofibroma and wound granulation of endothelial
cells e.g. intestinal adhesions, atherocal agent by reducing or
protein may also be useful as a birth control agent by reducing or
preventing uterine vascularisation. The gene for endostatin may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing uterine vascularisation. The gene for endostatin may be isolated from cells or tissue that express high levels of endostatin, etumour cells, by generating CDNA from mRNA using reverse transcriptase and then amplifying the DNA sequence.
Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                      The present sequence encodes an alternate functional endostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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100.0%; Pred. No. 0.058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 534 BP; 77 A; 189 C; 175 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 GACTICCAGIGCIICCAGCAGGCGCG 113
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                                                                                                                                                                              Claim 11; Page 40; 68pp; English.
                                              and angiogenesis, useful for
and as birth control agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 26; Conserv
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BP.

AAA27005 standard; DNA; 534

AAA27005

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The sequence encodes Human Endostatin(TM) N-terminal deletion mutant lacking the N-terminal 4 amino acids. The new method of the invention is useful for producing, recovering and purifying Endostatin (TM) from biological sources, such as biological fluids, tissues, cells, culture media, and fermentation media. Endostatin(TM) is useful for treating angiogenesis mediated diseases such as solid tumours, blood borne tumours, leukaemias, unuour metastases, benign tumours, e.g. haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis, coular angiogenic diseases, eg., diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, colon
                                                                                                                                                                            Human; Endostatin(TM); angiogenesis mediated disease; solid tumours; blood borne tumour; leukaemia; tumour metastasis; benign tumour; haemangioma; acoustic neuroma; neurofibroma; trachoma; rubeosis; pyogenic granuloma; rheumatoid arthritis; psoriasis; colon cancer; ocular angiogenic disease; diabetic retinopathy; macular degeneration; retinopathy of prematurity; macular corneal graft rejection; retinopathy of prematurity; macular forplasia; osler webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; mutant; ds.
                                                                                                                                            Human gene fragment encoding Endostatin(TM) N-terminal mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumours, comprises recombinantly producing the protein using an expression system, and recovering and purifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Variant produced during fermentation
reaction of Pichia pastoris harbouring an expression
plasmid containing the present sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partial
/note= "Neither of the above CDSs have start or stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang-Murad A, Zhou X, Madsen J, Boerner RJ; Y FR, Shepard SR, Schrimsher JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Endostatin(TM) N-terminal mutant#1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Endostatin(TM) N-terminal mutant#2'
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 32; 67pp; English.
                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-2000; 2000WO-US25166.
                                  AAS00868 standard; DNA; 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-244802/25.
P-PSDB; AAU00901, AAU00900.
                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codons"
                                                                                                                                                                                                                                                                                                                                                                                                                      .534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                        04-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-2001
                                                                    AAS00868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liang
RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
             AAS00868
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            myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilac joints, angiofibroma, and wound granulation. Endostatin(TM) is also useful for treating disease of excessive or abnormal stimulation of endothelial cells such as intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. Higher yields of more purified, and biologically active Endostatin(TM) are obtained by the new method. Endostatin(TM) can be stored in buffers for extended periods of time, and also subjected to lyophilisation, while preserving biological activity. Centrifugation of broth from fermentation steps in production is avoided, preventing unwanted potential cellular lysis and contamination with additional proteins, pigments, enzymes and other cellular chemicals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes an endostatin protein which is the carboxy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers and as birth control agents
                                                                                                                                                                                                                                                                                                                 Gaps
retrolental fibroplasia, rubeosis, Osler-Webber Syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endothelial cell proliferation inhibitor; collagen XVIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenesis inhibitor; anti-tumour; cytostatic; antipsoriatic; vasotropic, determatological; ophthalmological; vulnerary; antiarteriosclerotic; antiabetic; haemostatic; contraceptive; coular angiogenic disease; atherosclerosis; scleroderma;
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0
                                                                                                                                                                                                                                                                             DB 22; Length 537; 0.058;
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myocardial angiogenesis; telangiectasia; angiofibroma; wound granulation, ds.
                                                                                                                                                                                                                                            Sequence 537 BP; 79 A; 189 C; 176 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "Endostatin protein"
                                                                                                                                                                                                                                                                           4.7%; Score 26; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  88 GACTICCAGIGCTICCAGCAGGCGCG 113
                                                                                                                                                                                                                                                                                                                                                                    76 GACTTCCAGTGCTTCCAGCAGGGGG 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIL-) CHILDRENS MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA27004 standard; DNA; 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human endostatin gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY94323
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                                                                                                                                                                                                             debris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
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protein of human
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DB 21; Length 546; 0.057; 0; Indels Sequence 546 BP; 80 A; 196 C; 177 G; 93 T; 0 other; 4.7%; Score 26; DB 100.0%; Pred. No. 0.0; ive 0; Mismatches GACTTCCAGTGCTTCCAGCCGCGC 113 GACTTCCAGTGCTTCCAGCAGGCGCG 113 Query Match
Best Local Similarity 100.
Matches 26; Conservative 88

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AAX77719 standard; DNA; 549 BP. (first entry) 10-AUG-1999 AAX77719; RESULT 8 7777AA 

Human endostatin DNA coding region fragment.

Plasminogen; human; angiostatin; endostatin; gene therapy; vector; anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina; ss.

Homo sapiens

WO9926480-A1

03-JUN-1999.

20-NOV-1998;

98WO-US24950

97US-0975424 20-NOV-1997;

(GENE-)

GENETIX PHARM INC. MASSACHUSETTS INST TECHNOLOGY. (MASI)

Pawliuk RJ; Bachelot T, Leboulch P,

WPI; 1999-357696/30.

P-PSDB; AAY08693

Anti-angiogenic gene therapy vectors

Disclosure; Page 74; 83pp; English

nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiostatin, human or murine endostatin and angiogenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector This invention describes a novel viral gene therapy vector comprising a

88 GACTICCAGIGCITCCAGCAGGCGCG 113

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88 GACTTCCAGTGCTTCCAGCAGGCGCG 113

RESULT 10 AAZ51291

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes an angiogenesis inhibiting factor (1), designated IAF-1. The present invention also describes: (1) preparation of (1) and its derivative; (2) an IAF binding acceptor and its preparation; and (3) an IAF antibody. (1) is useful for preparing new biological preparations for effectively treating various tumours and abnormal-vessel diseases. The IAF antibody is preferably a polyclonal antibody, mosaic antibody, single stranded antibody and human originated
 expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiogenesis inhibiting factor 1 and its derivative useful for treating
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                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Human; angiogenesis inhibiting factor 1; IAF-1; tumour; antibody;
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anti-angiogenic polypeptide. An additional use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 549; 0.057;
                                                                                                         Length 549;
                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                    Human angiogenesis inhibiting factor 1 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
                                                                         Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ONCO-) INST ONCOLOGY UNDER TUMOR HOSPITAL CHINE.
                                                                                                         Score 26; DB 20;
Pred. No. 0.057;
                                                                                                 4.7%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
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100.0%; Pred. No. v.
0; Mismatches
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                                                                                                                                                                                                                                                                           AAA29884 standard; cDNA; 549
                                                                                                                                                                                                                                                                                                                                                                                                                    abnormal vessel disease; ss.
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                                                                                                       Query Match
Best Local Similarity 100.
Matches 26; Conservative
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Best Local Similarity
Matches 26; Conserv
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P-PSDB; AAY70252
                               WO200011033-A2.
                    Homo sapiens.
    06-JUN-2000
                                    25-AUG-1999;
                                       25-AUG-1998;
                                  32-MAR-2000
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'note= "None of the above CDSs have start or stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pyogenic granuloma; rheumatoid arthritis; psoriasis; colon cancer; ocular angiogenic disease; diabetic retinopathy; macular degeneration; retinopathy of prematurity; macular corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; Osler-Webber Syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Variant produced during fermentation reaction of Pichia pastoris harbouring an expression plasmid containing the present sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, Endostatin(TM), angiogenesis mediated disease, solid tumours, blood borne tumour, leukaemia, tumour metastasis, benign tumour, haemangioma, acoustic neuroma, neurofibroma, trachoma, rubeosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myocardial angiogenesis, plaque neovascularisation; telangiectasia;
haemophiliac joint; angiofibroma; wound granulation; ds.
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/product= "Endostatin(TM) C-terminus minus 1"
4.7%; Score 26; DB 21; Length 549;
100.0%; Pred. No. 0.057;
ive 0; Mismatches 0; Indels
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Bermejo LL, Mistry FR, Shepard SR, Schrimsher JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene fragment encoding Endostatin(TM) protein.
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/product= "Endostatin(TM)"
                                                                                                        88 GACTTCCAGTGCTTCCAGCAGGCGCG 113
                                                                                                                                                     88 GACTICCAGIGCTICCAGCAGGCGCG 113
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                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                     AAS00867 standard; DNA; 549
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                          Local Similarity 100.
nes 26; Conservative
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     Query Match
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Matches
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                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a signal sequence, an immunoglobulin For region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plaque neovascularisation, telangiectasia, haemophiliac joints angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis and Osler-Webber syndrome, myocardial angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of plasminogen fragment, however, the rest of the specification refers to this sequence as being nucleotide sequence of human endostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses a DNA molecule encoding a fusion protein comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin gamma (1gG) Fc fragment.
Note: This sequence is stated in claim 12 as being amino acid sequence
of plasminogen fragment, however, the rest of the specification
                                                                                                                                                                                                                                                                                   vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retinopathy; macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a cDNA encoding human endostatin used in the construction of immunofusin containing human
                                                                                                                                                                                                        Human; immunoglobulin gamma Fc fragment; endostatin; immunofusin; angjogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antipsoriatic; antidigbetic; ophthalmological; immunosuppressant; ansotropic; vulnerary; treatment; antiarteriosclerosis; tumour;
                                                                                                                                                                                                                                                                                                                                                             myocardial angiogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Does not include stop codon"
/partial
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                                                                                                                                                        Human angiogenesis inhibitor, endostatin cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Endostatin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..549
     AAZ51291 standard; cDNA; 549 BP.
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Boerner RJ;

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                                                                                                                                                                                                                                                borne tumours, leukaemias, tumour metastases, benign tumours, e.g.
haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic
granulomas, rheumatord arthritis, psoriasis, coular anglogenic diseases,
granulomas, rheumatord arthritis, psoriasis, coular anglogenic diseases,
c.g., diabetic retinopathy retinopathy of prematurity, macular
degeneration, corneal graft rejection, neovascular glaucoma, colon
cancer, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome,
myocardial anglogenesis, plaque neovascularisation, telangiectasia,
haemophiliac joints, anglofibroma, and wound granulation. Endostatin(TM)
is also useful for treating disease of excessive or abnormal stimulation
of endothelial cells such as intestinal adhesions, atherosclerosis,
cof endothelial cells such as intestinal adhesions, atherosclerosis,
scleroderma and hypertrophic sears. Higher yields of more purified, and
biologically active Endostatin(TM) are obtained by the new method.
Endostatin(TM) can be stored in buffers for extended periods of time, and
also subjected to lyophilisation, while preserving biological activity.
Centrifugation of broth from fermentation steps in production is avoided,
difficulty active minimanted protential cellular reference and other continual cellular reference and contained and charter and contained and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                additional proteins, pigments, enzymes and other cellular chemicals and
                                                                                                                                                                            invention is useful for producing, recovering and purifying Endostatin (TM) from biological sources, such as biological fluids, tissues, cells culture media, and fermentation media. Endostatin(TM) is useful for treating angiogenesis mediated diseases such as solid tumours, blood
                                 Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumours, comprises recombinantly producing the protein using an expression system, and recovering and purifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                             The sequence encodes Human Endostatin(TM). The new method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26; DB 22; Length 549;
Pred. No. 0.057;
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kringle domain; cell proliferation; viral vector;
replication-defective; cancer; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
P-PSDB; AAU00896, AAU00897, AAU00898, AAU00899
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/product= "Endostatin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endostatin coding sequence
                                                                                                                            Claim 6; Page 29; 67pg; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA00774 standard; cDNA; 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-2001; 2001US-287673P.
05-APR-2002; 2002US-370634P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-APR-2002; 2002WO-US13461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200288173-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA00774;
                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      debris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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This sequence encodes endostatin. Endostatin is a 20 kD C-terminal fragment of collagen XVIII that inhibits angiogenesis. The endostatin coding sequence may be used in the recombinant viral vector of the invention for obtaining angiostatin activity. The vector comprises a promoter capable of expressing human angiostatin operably linked to a structural gene encoding one or more domains of human angiostatin. The vector, which may be a replication-defective viral vector, is useful for inhibiting angiogenesis in a mammal, especially with cancer or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                             New recombinant viral vector expressing human angiostatin useful for inhibiting angiogenesis in a mammalian subject with cancer or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: This sequence is given incorrectly in the sequence listing of
the specification as an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endostatin; human; ophthalmological; ocular neovascularisation; choroidal neovascularisation; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
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/note= "the CDS does not include a start codon"
                                                 Mendez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
                                                 Jooss K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 25;
0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.7%; Scot.
100.0%; Pred. No. vo.
                                                 Patel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dixon KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 GACTICCAGIGCTICCAGCAGGCGCG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 GACTICCAGIGCTICCAGCAGGCGCG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product= "Endostatin"
                                                                                                                                                                                                                                                                Example 4; Page 80-82; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human endostatin coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ81193 standard; cDNA; 551 BP
                                                    Macarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brazzell RK, Campochiaro PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2002; 2002WO-US05336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2001; 2001US-270787P.04-APR-2001; 2001US-281296P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deery Match
Best Local Similarity 100.00
Best Local Similarity 100.00
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-2002 (first entry)
(CELL-) CELL GENESYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  partial/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..551
/*tag=
                                                                                                      WPI; 2003-129131/12.
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                                                    Wu WW,
                                                                                                                                 P-PSDB; AAG79753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200267971-A2
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                                                    Chang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour.
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Gregory SA;

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anti-anglogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           combinations of angiostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes multifunctional proteins which comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.7%; Score 26; DB 20; Length 552;
100.0%; Pred. No. 0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                         Casperson GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Limitarity 100.0%; Pred. No. 0.5 tes 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 GACTTCCAGTGCTTCCAGCAGGCGCG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 85; 121pp; English.
                                                                                                                                                                                                                                                                                                     MA, Caparon MH,
McKearn JP;
                                                                                                                        98WO-US20464.
                                                                                                                                                                                97US-0060609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC62023 standard; DNA; 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                         (SEAR ) SEARLE & CO G D.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-255098/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200060945-A1.
                                                                                                                                                                                                                                                                                                         Bolanowski MA,
                                                                                                                                                                                01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                        30-SEP-1998;
   WO9916889-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAR-2001
                                                               08-APR-1999
                                                                                                                                                                                                                                                                                                                                     Klein BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC62023;
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Matches
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ID AAC6
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   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       computation an endostatin-encoding nucleic acid. Cells secreting endostatin may be encapsulated and implanted within an individual. The method is used when ocular necvascularisation is caused by histoplasmosis, pathological myopia, angioid streaks, anterior ischaemic optic neuropathy, bacterial endocarditis, Best's disease, blidshot retinochoroidopathy, choroidal neamangioma, choroidal nonperfusion, choroidal neamangioma, choroidal neavi, choroidal nonperfusion, choroidal osteomas, choroidal nonperfusion, choroidal detachment, coloboma of retrapapillary bemartone of the retinal detachment, coloboma of the retinal pigmented epithelium, fundus flavimaculatus, idiopathic, macular hole, malignant melanoma, membranproliferative glomerulonephritis (type II), metalic intraocollar foreign body, morning glory disc syndrome, metalic intraocollar foreign body, morning glory disc syndrome, multiple evanescent white-dot syndrome, neovascularisation of ora serrata, operating microscope burn, optic nerve head pits, photocoagulation, punctate inner choroiditis, subretinal fluid drainage, tiled disc syndrome, Toxoplasma retinochoroiditis, tuberculosis, Vogt-Koyanagi-Harada syndrome, diabetic retinopathy, non-diabetic retinopathy, brain vein occlusion, retinopathy, brain vein occlusion, retinopathy, brain vein occlusion, retinopathy, brain vein occlusion, retinopathy, retinal cryoinjury, retinitis pigmentosa, retinopathy, retinal cryoinjury, retinitis pigmentosa, retinopathy, retinal cryoinjury, retinitis pigmentosa, retinopathy, resinal cryoinjury, retinitis pigmentosa, retinopathy, resinal cryoinjury, retinitis pigmentosa, retinopathy, resinal corneal ulcers, retinopathy menacinal pretinitis simple simple.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                   The present sequence is a partial coding sequence for human endostatin. A claimed method for the treatment of ocular neovascularisation, especially choroidal neovascularisation, involves increasing the level of endostatin in ocular tissue, especially where the endostatin is encoded by the present sequence, or is its fragment, derivative or variant. The increase is effected by administering a viral vector, especially an adenovirus, adeno-associated virus, a retrovirus or lentivirus vector,
                                                        Treating or preventing choroidal neovascularization comprises increasing the amount of endostatin in ocular tissues of afflicted individuals to a choroidal neovascularization inhibiting level -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interferon-inducible protein; platelet factor 4; anti-anglogenic; anti-tumor; multifunctional protein; anglogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiostatin; endostatin; interferon; thrombospondin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 551 BP; 83 A; 195 C; 179 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      keratoplasty, pterigyia and trauma (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 GACTICCAGIGCTICCAGCAGGCGCG 113
                                                                                                                                                                             Claim 27; Page 39-40; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX35375 standard; DNA; 552 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID 50 of WO9916889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
P-PSDB; ABB79901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX35375;
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Gaps

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0; Indels

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Nucleotide sequence of human endostatin encoded by plasmid pMALcH#15.
                                                                                                                          Streptomyces sp. strain C5; SnpA; S. venezuelae; alpha-amylase;
endostatin; cancer; tumour growth; angiogenesis; ss.
88 cacriccacriccaccaccacccc 113
                                                                                                                                                                                                     "endostatin"
                                                                                                                                                                          Location/Qualifiers
                                                BP.
                                                                                                                                                                                                                                                              12-APR-2000; 2000WO-US09747
                                                                                                                                                                                                                                                                                 99US-0129084
                                                                                                                                                                                                                                                                                 13-APR-1999;
                                                                                                                                                                                                                                           19-OCT-2000.
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tumor cell production; ss.

RESULT 14 AAX35375

Matches

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Homo sapiens

(MERI ) MERCK & CO INC.

Desanti CL, Strohl WR;

WPI; 2000-686970/67.

P-PSDB; AAB30493

Preparation of soluble recombinant endostatin involves transforming Streptomycete host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader peptide

Example 1; Fig 6; 57pp; English.

in Streptomyces. Leader sequences of Streptomyces sp. strain CS snpA and S. venezuelae alpha-amylase proteins are linked to the sordered as a secreted, soluble protein which needs no refolding, is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer, inhibition of tumour growth, inhibition of angiogenesis, isolation of receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced. The present sequence encodes human endostatin. The protein is expressed 

Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;

Gaps ö 4.7%; Score 26; DB 21; Length 552; 100.0%; Pred. No. 0.057; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 26; Conservative Query Match

88 GACTTCCAGTGCTTCCAGCAGGCGCG 113

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88 GACTTCCAGTGCTTCCAGCAGGCGCG 113

Search completed: August 17, 2003; 16:43:15 Job time : 214.14 secs

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APPLICANT: Abitbol, Marc
APPLICANT: Uteza, Yves
APPLICANT: Uteza, Yves
APPLICANT: Uteza, Yves
APPLICANT: Wenselve, Maurice
APPLICANT: Bonsel, Sebastien
APPLICANT: Bonnel, Sebastien
APPLICANT: Bonnel, Sebastien
APPLICANT: Prats, Herve
APPLICANT: Prats, Herve
APPLICANT: Neumer-Jehle, Martin
APPLICANT: Neumer-Jehle, Martin
APPLICANT: Neumer-Jehle, Martin
APPLICANT: Bornel, Jiri
APPLICANT: Neumer-Jehle, Martin
APPLICANT: Neumer-Jehle, Jiri
APPLICANT: Neumer-Jehle,
TITLE OF INVENTION: INTRACCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.2020801
CURRENT FILING DATE: 1999-11-24
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Horiger, Jiri
APPLICANT: Horiger, Jiri
APPLICANT: Neuner-Jehle, Martin
TITLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.2020201
CURRENT APPLICATION NUMBER: US/09/775,325
CURRENT FILING DATE: 2001-02-01
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 558
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                                         Length 292;
                                                                                       Indels
                                         Score 18; DB 3;
Pred. No. 56;
                                                                                    Mismatches
                           3.2%; SCC.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09775325
Patent No. 6500449
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abitbol, Marc
APPLICANT: Uteza, Yves
APPLICANT: Menasche, Maurice
APPLICANT: Bossard, Carine
APPLICANT: Van Den Berghe, Loic
APPLICANT: Bonnel, Sebastian
APPLICANT: Prats, Herve
                                                                                                                                                                                                                                                              US-09-449-293-3; Sequence 3, Application US/09449293; Patent No. 6267954
                                                                                                                                127 GCCGGCACCTTCCGGGCC 144
                                                                                                                                                                            235 GCCGGCACCTTCCGGGCC 218
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                                                                                       Conservative
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; ORGANISM: Rattus rattus
US-09-775-325-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Rattus rattus US-09-449-293-3
                                       Query Match
Best Local Similarity
Matches 18; Conserv
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Matches 18; Conserv
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US-08-956-307B-9
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LENGTH: 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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100.0%; Pred. No. 56;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,307B
FILING DATE: 22-OCT-1997
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Petka, Wendy A.
APPLICANT: Tirrell, David A.
APPLICANT: Kevin P. McGrath
TITLE OF INVENTION: REVERSIBLE HYDROGELS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07880/033001
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US-08-956-307B-9/c
Sequence 9, Application US/08956307B
Patent No. 6090911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GCCGCCACCTTCCGGGCC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                32,983
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                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ 1D NO: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 292 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        single
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
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02110-2804
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TYPE: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-04-2
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 573
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Best Local Similarity 100.
Matches 18; Conservative
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Best Local Similarity 100.
Matches 18; Conservative
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; LOCATION: (1)..(573)
US-09-561-108-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Pat
SEQ ID NO 12
LENGTH: 573
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                                                                                                                                                                                                                                                                                                         APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1220 Market Street, P.O. Box 2207
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Patent No. 6342219
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTHEODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002500
CURRENT FILING DATE: 2000-04-38
PRIOR APPLICATION NUMBER: 60/131,432
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                       Length 558;
                                                               0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
          3.2%; Sco...
100.0%; Pred. No. ...
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100.0%; Pred. No.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/ARBIT INFORMATION:
NAME: MCMOSTYOW JT., ROBERT G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              Sequence 37, Application US/08985526 Patent No. 6080728
                                                                                                                                              313 GACGGCAGAGATGTCCTG 330
                                                                                                      310 GACGCCAGAGATGTCCTG 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (302) 658-914
TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 565 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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nes 18; Conservative
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Mixson, Ji
TITLE OF INVENTION:
TITLE OF INVENTION: I
                     Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Wilmington STATE: Delaware
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US-09-561-500-12
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Best Local S
Matches 18
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Sequence 12, Application US/09561108
Patent No. 634221
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Breken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/561,108
CURRENT FILING DATE: 2000-04-28
RIOR PALICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIN Ver. 2.0
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Sequence 12, Application US/09561526
Sequence 12, Application US/09561526
Sequence 12, Application US/09561526
GENERAL INFORMATION:
APPLICANT: POLITY B. Thorpe
APPLICANT: ROLF A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002566
CURRENT FILING DATE: 2000-04-28
RIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATCHIN Ver. 2.0
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
OTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
LOCATION: (1)..(573)
US-09-561-500-12
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52;
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100.0%; Pred. No. ...
0; Mismatches
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100.0%; Pred. No. ....
0; Mismatches
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Patent No. 6524583

GENERAL INFORMATION: 3

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TILE OF INVENTION: ANTHOON METHODS FOR SELECTIVELY INHIBITING VEGF

FILE REFERENCE: 4001.002582

CURRENT APPLICATION NUMBER: US/09/561,499

CURRENT FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 573
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                                                                                           FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
NOTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KRY: CDS
LOCATION: (1) ..(573)
US-09-561-526-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC;
NOTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
LCCATION: (1)..(573)
US-09-561-499-12
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APPLICANT: Petka, Wendy A.
APPLICANT: Tirrell, David A.
APPLICANT: Kevin P. McGrath
TITLE OF INVENTION: REVERSIBLE HYDROGELS
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08956307B Patent No. 6090911
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ORGANISM: Artificial Sequence
                                                  TYPE: DNA ORGANISM: Artificial Sequence
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STATE: MA
COUNTRY: USA
ZIP: 02110-2804
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US-08-956-307B-12
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US-09-561-499-12
SEQ ID NO 12
LENGTH: 573
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatable
CORRATING SYSTEM: Windows 95
SOFTWARE: FastSEG for Windows Version 2.0b
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/956,307B
PRILING DATE: 22-0CT-1997
PRILING DATE: 22-0CT-1997
PRILING DATE: 32-0CT-1997
PRILING DATE: 32-0CT-1997
PRILING DATE: 32,983
REPERRENCE/DOCKET NUMBER: 32,983
REPRENCE/DOCKET NUMBER: 32,983
REPERRENCE/DOCKET NUMBER: 32,983
REPRENCE/DOCKET NUMBER: 32,983
REPERRENCE/DOCKET NUMBER: 32,983
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CB216999 NISC MG1
BM768821 K-EST0651
BM683067 UI-B-E01-
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BE908201 G01500458
CB443805 694911 MA
AU125614 AU125614
BE906253 60150237
BE906253 60150237
BC387051 602454749
BU540812 AGENCOURT
BU540812 AGENCOURT
BU540812 AGENCOURT
BU5404034 AGENCOURT
BU944034 AGENCOURT
BU954034 AGENCOURT
BU956872 AGENCOURT
BU956872 AGENCOURT
BU956873 AGENCOURT
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CB796474 AMGNNUC:S
CB716008 AMGNNUC:N
BIZ88582 UI-R-DK0-
BM488074 pgm2n.pk0
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AI809446 wf70g07.x
BQ897787 AGENCOURT
BU227326 603798785
BB187708 BB187708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW464343 linear EST 24-FEB-2000 BP230015B10C11 Soares normalized bovine placenta Bos taurus CDNA clone BP230015B10C11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
          CB424313 598557 MA
BF708656 MI-P-AY0-
BG383960 302432 MA
BG383970 302444 MA
                                                                   AV660284 AV660284
BF602228 267408 MA
BG323096 602726433
AV727686 AV727686
AV727879 AV727879
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Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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                                                                   AV660284
BF602228
BG823096
AV727686
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BQ723254
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BI288582
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Bos taurus
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BF074459 221883 MA
CB444165 695295 MA
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8338.472 Million cell updates/sec
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                                                                                                                                                                                            552
                                                                                                   August 17, 2003, 16:23:08 ; Search time 1617.68 Seconds
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(c) 1993 - 2003 Compugen Ltd.
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                                                                        - nucleic search, using sw model
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seq length: 200000000
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Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: cross_match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length.
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/close_lb="Soares normalized bovine placenta" | Colose_lb="Soares normalized bovine placenta" | Site_2: Not1; The CDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F. Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
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100.0%; Pred. No. 3.4e-11;
iive 0; Mismatches 0; Indels
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
T=1: 402 762 4390
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                        FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 279 Std Error: 0.00
Plate: BP230019B10 row: C column: 11
Seq primer: AGCGGATAACAATTCACACGA
High quality sequence stop: 279.
                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="BP230015B10C11"
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FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
vo.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
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                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made_from pooled tissue_from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
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/db_xref="teaxon:9913"
/tissue type="pooled"
/lab_host="poled"
/lab_host="DH10B"
/clone_lib="MARC_2BoV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
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221883 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BF074459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.5%; Score 47; DB 10; I
100.0%; Pred. No. 3.5e-11;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .551
/organism="Bos taurus"
Plate: 40 row: H column: 7
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                   /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACCAGG
Plate: 81 row: F column: 9
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Conservative
                                                                                                                                                1. .387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (cow)
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
Do Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
plate: FQY8006 row: I column: 12
Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                                                                                                                                        Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
Eximal with the aid of the trim_alt option. Vector identified with
Cross match v0.990329.
                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos.
1 (bases I to 409)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Dages 1 to 623)
Smith T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
Mray, J.E. and keele, J.W.
A second set of bovine BSTs from pooled-tissue normalized libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab.host="pooled"
/clome_lib=mARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB424313 623 bp mRNA linear
598557 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.
CB424313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.6%; Score 31; DB 14; Lilarity 100.0%; Pred. No. 0.00098; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 TGCCCGTCGTCAACCTCAGGGACGAGGTGCT 236
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                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: LAM8036 row: F column: 23 Seg primer: TAGAAGGCACAGTCGAGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9913"
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  Bos taurus (cow)
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tes 31; Conserv
                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SOURCE
ORGANISM
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                    ORGANISM
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COMMENT
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JOURNAL
COMMENT
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                                                                                                        REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
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Smith,T.P.L., Roberts A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
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                                                                                                                                                                                                                                                                                                                                                        EST 25-MAR-2003
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /_clone_lib="MARC 6BOV"
//clone_lib="MARC 6BOV"
//note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
-Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
                                                                                                                                                       Gaps
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semitendonosus muscle, longissimus muscle, pancreas,
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                                                                                                                                                                                                 94 CAGTGCTTCCAGCAGGCGCGCGCGCGGGGCTGGCCGGCACCTTCCG 140
                                                                                                                                                                                                                      70 CAGTGCTTCCAGCAGGCGCGCGCGCGGGCTGGCTGCCGCACCTTCCG 116
                                                                                                    8.5%; Score 47; DB 10; Length 551;
100.0%; Pred. No. 3.6e-11;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%; Score 41; DB 14; Length 657;
100.0%; Pred. No. 2.3e-08;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB537919 409 bp mRNA linear 775852 MARC 6BOV Bos taurus cDNA 3', mRNA sequence. CB537919.1 GI:29406863
                                                                                                                                                                                                                                                                                                                                                        CB444165 GBOV BOS taurus cDNA 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643 CAGTGCTTCCAGCAGGCGCGCGCGCGGGGCTGGCCGGCAC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: FQY8051 row: I column: 11 Seq primer: TAGAAGGCACAGTCGAGG.
                       adrenal, and endometrium.
1 200 c 179 g 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
/mol_type="mRNA"
/db_Xef="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                            CB444165.1 GI:29233914
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                                                                                                                                                     47; Conservative
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                                                                                                        Query Match
Best Local Similarity
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DEFINITION
ACCESSION
VERSION
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CB444165/c
LOCUS
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CB537919/c
                                       BASE COUNT
ORIGIN
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JOURNAL
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AUTHORS
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KEYWORDS
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FEATURES

ORIGIN

8

COMMENT

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Gaps

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Length 409;

EST 25-MAR-2003

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please visit our web site at
                                                                                                                                                                                          5.2%; bcc.
100.0%; Pred. No. c.
0; Mismatches
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                                                                                                                                             84 t
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                                                                                                                                                                                                                                                                                   292 GCCCGCATCTTCTTTCGACGCAGAGA 320
                                                                                                                                                                                                                                                                                                                         340 gcccgcarcrrcrcrrrcgacgcagga 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mamm. Genome 13 (8), 475-478 (2002) 22213789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: AGGAACAGCTATCACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 89 row: I column: 13
Seg primer: ATTTAGGGGGACACTATAG.
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153 c 15
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                                                                                                                          TAG_SEQ=ATTGG"
109 c 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
                                                                                                                                                                                                                                            29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (pig)
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa
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                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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VERSION
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PUBMED
COMMENT
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BG383960
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                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 bp mRNA linear EST 02-JAN-2001 MI-P-AYO-ncq-g-09-0-UI.sl MI-P-AYO sus scrofa cDNA clone MI-P-AYO-ncq-g-09-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: oktuggle@lastate.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized placenta library cDNA Library Preparation: M.B. Soares Lab, University of Iowa ESI sequencing: M.B. Soares Lab, University of Iowa Clone distribution: clones will be available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MI_P-AXO-ncq-g-09-0-UI"
/lab.host="MI_P-AXO"
/clone lib="MI-P-AXO"
/note="Wector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: EcoRI; Fhe MI-P-AXO
library is derived from placenta. For a detailed
description of the library from which this clone was
                                                                                                                                        /clone lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tIssues
including liver; lung, hypothalamus, pituitary, and
placenta/endometrium.
199 c 193 g 126 t
                                                                                                                                                                                                                                                                                                                                              Gaps
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Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
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                                                                                                                                                                                                                                                                                                    5.6%; Score 31; DB 14; Length 623;
100.0%; Pred. No. 0.001;
ive 0; Mismatches 0; Indels
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Seg primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                     206 TGCCCGTCGTCAACCTCAGGGACGAGGTGCT 236
                                                                                                                                                                                                                                                                                                                                                                                                            572 TGCCCGTCGTCAACCTCAGGGACGAGGTGCT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
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/mol type="mRNA"
/db_xref="taxon:9823"
                                                            /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                           organism="Bos taurus"
    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                              31; Conservative
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Fax: 5152942401
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KEYWORDS
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TITLE
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PUBMED
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    FEATURES
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http://pigest.genome.iastate.edu/. The procedure used to create this library has been previously described (Bonaldo , Lennon and Soares, Genome Research 6:791-806, 1996)
TAG LIBB-T-P-AT
TAG_ITISSUE=placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Mammalia; Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1 (bases 1 to 451)
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/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_bnost="PH10B"
/clone_lib="WARC_IPIG"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
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                                                                                                                                                                                                                                                                  Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG383960 451 bp mRNA linear 302432 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
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Fax: 402 762 4390
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0.0082;
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovidae; Bos.

1 (bases 1 to 408)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wary, J.B., White, J., Chall, Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 25-APR-2001
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Aban, K., Lul, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="corresponding non cancerous liver tissue"
/dev stage="Adult"
/lab_host="SOLR"
/clone lib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                 Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc:sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.7%; Score 26; DB 9; Length 390; 100.0%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF602228 408 bp mRNA linear 267408 MARC 3BOV BOS taurus CDNA 5', mRNA sequence.
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4390
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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ACCESSION
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PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                               Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J. and Keele, J.W.

Borchne gene discovery by normalized cDNA-library sequencing and EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 370)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="MARC 1PIG"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                             mRNA linear
5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 t
  112 GCCCGCATCTTCTTTCGACGCCAGAGA 140
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                                                                                                             BG383970
302444 MARC 1PIG Sus scrofa cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
Plate: 89 row: K column: 13
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9823"
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                           Sus scrofa (pig)
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Gaps

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/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
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   68
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/db_xref="taxon:9606"
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Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="HTCASB12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hanzg@chgc.sh.cn
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EST.
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nes 26; Conservative
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//MOJ_type="mRNA" Captons
//MOJ_type="mRNA" Captons
//MOJ_type="MRNA" Captons
//Lissue_Lype="Manocarcinoma cell line"
//Lissue_Lype="Manocarcinoma cell line"
//Lishost="MILOB (phage-resistant)"
//Lishost="MILOB (phage-res
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602726433F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4865936 5',
                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/tissue_type="pooled"
/tab_host="DH10B"
/clone_lib="WARC 3Bov"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longigatus muscle."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 483)
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Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMA732 row: a column: 09
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National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 479.
Location/Qualifiers
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   PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 43 row: D column: 15
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                          organism="Bos taurus"
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Best Local Similarity 100.
Matches 26; Conservative
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 485)

Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X., Gi, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.

Unpublished
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                           AV727686 AV27686 485 bp mRNA linear EST 17-OCT-2
AV727686 HTC Homo sapiens cDNA clone HTCASB12 5', mRNA sequence.
                                                                      Gaps
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                DB 12;
0.21;
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Pred. No. 0.21;
4.7%; Sco...
100.0%; Pred. No. c...
0; Mismatches
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Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM13167 row: F column: 11
               Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu
,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S56 bp mRNA linear EST 06-FEB-2003 NISC_nq11c06.y1 NICHD_HS_Ut2 Homo sapiens cDNA clone IMAGE:5938570 CB216999
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1 (bases 1 to 556)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National.Gancer Institute, Cancer Genome Anatomy Project (CGAP);

Tumor Gene Index

Unpublished
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                          Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
251 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. Sec. 21-50801919 (ex.45)
Tel: 86-21-50801992
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cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                 Email: harzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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Seq primer: M13RP1 reverse primer (ABI)
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4.7%; Score 26; DB 9;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 26; Conservative 0; Mismatches
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dev_stage="Adult"
lab_host="SOLR"
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/mol_type="mRNA"
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/clone="HTCARG03"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5938570"
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/lab_host="milloB (T1-resistant)"
/clone_lib="NICHD HS Ut2"
/note="Organ: uterus; Vector: pCMV-SPORT6.1.ccdb (ResGen, Invitrogen Corporation); Site_1: NotI; Site_2: BCORV;
Cloned unidirectionally from microquantity amounts of mRNA from normal endometrial tissue (mid-secretory phase, cycle day 23). Average insert size 1.6 kb. Library constructed by ResGen (Invitrogen Corporation).

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Job time : 1619.68 secs
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ion	AX399631 Sequence AX399629 Sequence BC033715 Homo sapi AR193165 Sequence AX300086 Sequence AX473815 Sequence AX473815 Sequence BD081407 Fused pro AR282883 Homo sapi AX4708511 Sequence AX6098216 Homo sapi AR193165 Sequence AX137082 Sequence AX137082 Sequence AX137082 Sequence AX137082 Sequence AX100092 Sequence AX100092 Sequence AX137083 Sequence AX108406 Sequence BB102800 Process f BB128313 Endostati AR26809 Sequence AX137083 Sequence AX128409 Sequence AX2775 Mus musculu BC043697 Mus musculu BC043697 Mus musculu AX128409 Sequence AX27775 Mus musculu AX28409 Sequence AX27775 Mus musculu AX28409 Sequence AX27775 Mus musculu AX28409 Sequence AX368771 Sequence AX287775 Mus musculu AX28409 Sequence AX368778 Ratus no AR88350 Sequence AX368778 Axtus musculu AX287775 Mus musculu AX287775 Mus musculu AX287775 Mus musculu AX287775 Mus musculu AX388778 Sequence AX368771 Sequence AX368771 Sequence AX368771 Sequence AX368771 Sequence AX368773 Ratus no AR88771 Sequence AX368773 Ratus no AR88771 Sequence AX368773 Ratus no AR88773 Ratus no AR88773 Ratus no AR88773 Ratus no AR88773 Ratus no AX490866 Sequence AX368774 Ratus no AR88773 Ratus no AX490866 Sequence AX368774 Ratus no AX698774 Ratus no AX698740 Gallus ga	DD DNA linear PAT 06-JUN-2002 036. Craniata; Vertebrata; Euteleostomi; ; Fissipedia; Canidae; Canis. diagnosing and treating disorders
SUMMARIES	AX399631 AX399629 BC033715 AX100086 AX4798662 AX479862883 AX4798831 BD081407 AZ428883 AX3708531 AX3708621 AX370862 AX370862 AX370862 AX370862 AX370862 AX100642 AX100642 AX100642 AX100642 AX10064406 AX1006420 AX1006406 AX10064106 AX10064106 AX10064106 AX10064106 AX10064106 AX10064106 AX12409 IS1044 MUSCOLLAG AX183520 AR21775 AR21775 AR21775 AR21775 AR2183520 AX210666 RNO236873 AR217775 AR217775 AR217775 AR2183520 AR217775 AR2183520 AR217775 AR2183520 AR217776 AR217776 AR2183520 AR217776 AR2177776 AR21777777777777777777777777777777777777	555 P1191 data; ivora
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Res	<b>!</b>	REE CONTRACTOR

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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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BC033715.1 GI:21708148
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Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
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Methods and compositions for diagnosing and treating disorders involving angiogenesis
Patent: EP 1191036-A 1 27-MAR-2002;
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/mol_type="genomic DNA"
/db_xref="taxon:9615"
Patent: EP 1191036-A 3 27-MAR-2002; Pfizer Products Inc. (US)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (02-701-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
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Homo sapiens, Similar to collagen,
IMAGE:4425380, mRNA, partial cds.
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2382 AGTGCCGCGAGCTGCCATCACGCCTACATGTGCTCTGCATTGAGAACAGCTTCATGACT 2441
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                                                                                CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC
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Patent: US 6346510-A 4 12-FEB-2002;
Location/Qualifiers
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O'Reilly,M.S. and Folkman,M.Judah.
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Sequence 4 from patent US 6346510.
AR193165.1 GI:20239130
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85.3%;
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                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK plate: 68 Row: e Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing, Maryland;
Sequencing, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Gun,X., Gupta,J., Haghighi,P.,
Dietrich,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LWATROAMLGGVHEVPEGWLIFVAEQEELYVRVQNGFRKVQLEARTPLPRGTDNEVAA
LOPPVVQLIHDSNPYPRREHPHTARFWRADDILASPBRLPEPOPYGAPHHSSYVHLR
PAR PTSPPAHSHRDFQPVLHLVALNSPLSGGMRGIRGAFOCEQQARAVGLAGTRAF
LISSRLQDIYS I VRRADRAAVPIVNLKDELLPSWEALFSGSEGPLKPGAR I FSEDGKU
VLRHPTWPQKSVWHGSDPNGRRLIFSSYCETWRTEAPSATGQASSLLGGRLLGGSAASC
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GPPG1GYEGRQGPPGPPGPPSFPGPHRQT1SVPGPPGPPGPPGPPGTWGASSGVR
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                Tissue Procurement: ATCC COND Life Technologies, Inc. CDN Library Preparation: Life Technologies, Inc. CDN Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing Dy: National Institutes of Health Intramural Sequencing Center (NISC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:4425380"
/tissue_type="Kidney, hypernephroma"
/clone_lib="NHH_MGC_89"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Email: cgapbs-r@mail.nih.gov
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TTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCACCTGGCCCCAGAAGAGCGTGTGG 360
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                         421 GAGGCTCCCTCGGCCACGGCCTCCTCGCTGCTGGGGGGGCAGGCTCCTGGGGCAG
                                                                                                                                                          481 AGGCCGCGAGCTGCCATCACGCCTACATCGTGCTTCTGCATTGAGAACAGCTTCATGACT
                                                                                     GAGGCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGCTGGCGGGCAGGCTGCTGGAGCAG
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Angiostatin and endostatin binding proteins and methods of
Patent: WO 0193897-A 30 13-DEC-2001;
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Sequence 30 from Patent WO0193897.
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Pred. No. 1
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
_196 c 179 g 9
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Location/Qualifiers
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Best Local Similarity 85.3%;
Matches 466; Conservative 0
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Patchod of producing and purifying endostatin?tm protein Patent: WO 0119989-A 4 22-MAR-2001;
EntreMed, Inc. (US)
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E 2 (abanowski, M.A., Caparon, M.H., Casperson, G.F., Gregory, S.A., Klein, B.K. and Mckearn, J.P.

Klein, B.K. and Mckearn, J.P.

Klein, B.K. and Mckearn, J.P.

Klein, B.K. and utilization therapy

Puse of protein containing angiostatin component and utilization thereof in antitumor therapy

Batent: JP 2001518304-A 50 16-OCT-2001;

GD SHARLE AND CO

OS Homo sapiens (human)

PN JP 2001518304-A/50

PP 30-SEP-1999 JP 2000513958

PR 01-OCT-1997 US 60/060609

PI MARK A BOLANOWSKI, MAIRE H. CAPARON, GERALD F. CASPERSON, SUSAN A PI GREGORY,

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PC CLIZNIS/09, A61K38/00, A61K48/00, A61P9/10, A61P35/00, CO7K14/52, PC
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Fused protein containing angiostatin component and utilization
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C12N15/09,A61K38/00,A61K48/00,A61P9/10,A61P35/00,C07K14/52, PC
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Angiogenesis-inhibiting peptides and proteins and methods of use
Patent: WO 0230983-A 2 18-APR-2002;
EntreMed, Inc. (US)
Location/Qualifiers
                                                                           481 GAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC
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/organism="synthetic construct
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="mRNA for mIgSP fused to
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Homo sapièns multi-functional protein MFP mRNA, complete cds.
AF282883
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/protein id="AAM52249.1"
/db_xref="G1:21425751"
/translation="MSEGNSGGSGGGGVITKIKGGGSGGGSGGGRNPDGDAKPWGGG
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Submitted (27-JUN-2000) R & D, Robinson Biotech Corp., 24634 Five
Mile Road, Suite 24-26, Redford, MI 48239, USA
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/codon_start=1
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                   Length 2364;
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Pred. No. 1.2e-46;
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Sequence 2178 from Patent WO0229103.
                                                                                                                                                                                                                             0, Mismatches
/db_xref="taxon:9606"
/clone="UTERU2002964"
/tissue_type="uterus"
/clone_lib="UTERU2"
/note="cloning vector: p'
a 768 c 776 g 40
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/mol_type="genomic DNA"
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AX409531.1 GI:21442236
                                                                                                                                                                                Query Match
Best Local Similarity 85.3%;
Matches 466; Conservative
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
CB-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Gonomoy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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highly similar
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                    GTGCGCCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC
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2364 bp mRNA linear Homo sapiens cDNA FLJ40897 fis, clone UTERU2002964, to Homo sapiens type XVIII collagen (COL18A1) mRNA.
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AK098216.1 GI:21758185
oligo capping; fis (full insert sequence)
Homo sapiens (Auman)
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NEDO human cDNA sequencing project
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gai, T. and Yamamoto, J.
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS

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RESULT 11 AK098216 ACCESSION

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PEATURES

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PAT 14-JUN-2002

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'organism="Homo sapiens
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1. .3394
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alpha-1 type XVIII collagen.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                  1504 CACAGCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCA 1563
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Pred. No. 1.1e-46;
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Pred. No. 1.1e-46;
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          /nore="EMBL/GenBank Accession No. L22548"
1130 c 1080 g 516 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 3394)
Olsen, B.R. and Oh, S.P.
Collagen and uses therefor
Patent: US 5643783-A 4 01-JUL-1997;
Location/Qualifiers
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Sequence 4 from patent US 5643783.
151045
/db xref="taxon:9606"
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1130 c 1080 a
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                                                           75.3%;
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Matches 466; Conservative
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                    1130 c
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Best Local Similarity 85.3
Matches 466; Conservative
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HUMCOL18AX 3394 bp mRNA linear PRI 01-NOV-1994
Human collagen type XVIII alpha 1 (COL18A1) mRNA, partial cds.
L22548
                                       1504 CACAGCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCA 1563
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1 (baess 1 to 3394)
10h, S.P.; Warman, M.L.; Seldin, M.F.; Cheng, S.D.; Knoll, J.H.; Timmons, S. and Olsen, B.R.
Cloning of cDNA and genomic DNA encoding human type XVIII collagen and localization of the alpha 1(XVIII) collagen gene to mouse chromosome 10 and human chromosome 21
Genomics 19 (3), 494-499 (1994)
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9
                                                                                                                                                                                                                                                   GGGCTGGCCGCCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC
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Location/Qualifiers
1. .3394
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AF018082.1 GI:2920536
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Matches 466; Conserva
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Homo sapiens type XVIII collagen (COL18A1) mRNA, alternatively
Spliced, short form, complete cds.
                                                                                                                                                                                              GGFFGSSLFCAPGAPGPRGYPGIPGFKGESIRGQPPGPPGGPPGIGYEGRQGPPGPP
PPGPPSPFSPCPHRQTISVPGPPGPPPGPPGPFGTAGASSGOVERMATROAMGOVHEVP
EGWLIFVAEOGELYKRQNGFRKVQLEARTPLPRGTDNEVAALQPPVVQLHSNPYPR
REHPHPTARPWRADDILASPPGLPEPQPYPGGPHHSSYVHCGPARPTSPPAHSHRDFQ
                                                                                                                                                                                                                                                                     PVLHLVALNSPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRAD
RAAVPIVNLKDELLFPSWEALFSGSEGPLKFGARIFSFDGKDVLRHPTWPQKSVWHGS
DPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSFWTA
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LPGNQGPPGPKGEVGPPGPPGQFPFDFLQKEAEMKGEKGDRGDAGQKGERGEPGG
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PGPKGEKGEPGSIFSPDGGALGPAQKGAKGEPGFRGPPGLYGRPGYKGEIGFPGRPGR
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                                                  /product="collagen type XVIII alpha 1"
/protein id="AAA51864.1"
/db_xref="GI:562794"
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DEFINITION

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5408)
Saarela,J., Ylikarppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T. Complete primary structure of two variant forms of human type XVIII collagen and tissue-specific differences in the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOLIGOPPPQQYTQTDDPDVGLAYVPGPDANSGQVARYHFPSI.FFRDFSLI.FHIRPAT
EGPGYLFAITDSAQAAVLLGYKLSGVQDGHQDISLIYTEPGAGCYTHTAASFRLPAFVG
QWTHLALSVARQGFVALYVDCEFFQMPLARSSRGLELEPGAGLFVAQAGGADPDKFQG
VIAELKYRRDPQVSPWHCLDEEGDDSDGAFGFGDSGGGGDARELLREETGAALKPRLPA
PPPVTTPPLAGGSSTEDSRSEEVEEQTTVASLGAQTLPGSDSVSTWDGSVRTPGGRVK
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ATRQAMLGQVHEVPEGWLIFVAEQEELYVRVQNGFRKVQLEARTPLPRGTDNEVAALQ
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RHPTWPQKSVWHGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHH
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                                                                                                                                                                                                                                                                                                  2 (bases 1 to 5408)
Saarela,J., Ylkarppa,R., Rehn,M., Purmonen,S. and Pihlajaniemi,T.
Direct Submission
Submitted (28-UIL-1997) Dept. of Medical Biochemistry, University
of Oulu, Kajaanintie 52 A, Oulu 90220, Finland
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/note="alternatively spliced; short form (NC1-303)"
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Pred. No. 9.1e-47;
0; Mismatches 80
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                                                                                                                                                                                              corresponding transcripts
Matrix Biol. 16 (6), 319-328 (1998)
98164096
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/db_xref="GI:2920537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .5408
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
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3639 GGGCTGGCGGCCATCCTGCCTGCCTCCCGCCCTGCAGGACCTGTAGAGCATC 3698

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        GTGCGCCGCCCGCCCGCCCGTCGTCGTCAACCTCAGGACGACGAGGTGCTCTTC
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        3699
        GTGCGCCGTCGCGCGCGCGCGCGCCGTCGTCGTCAAGGACGAGCTGCTGTTT
        3758

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                                                                                                                                                                                                                                                                                                                                                           3879 CATGGCTCGGACCCCAACGGCGCAGGCTGACCGAGAGCTACTGTGAGACGTGGCGGACG 3938
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3939 GAGGCTCCCTCGGCCACGGCCTCCTCGCTGCTGGGGGGCAGGCTCCTGGGGCAG 3998
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                                                                                                                                                                                                                                                                                                                                  420
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Search completed: August 17, 2003, 15:15:32 Job time: 2789.13 secs

DNA encoding a hum Synthetic plasmid Nuclectide sequenc Human alpha-1 coll Human alpha1 (XVII Gene #2178 used to Human pancreatic C

AAA64013 ABK09977 AAC62025 AAT84484

ABN95680 ABV94763 ABN85301

ABQ54955

33394 33394 45594 45591 48551 5408 551 641 641

Human endostatin c Human endostatin c

CDNA encoding huma

Human vascular end

Human endostatin c

Human endostatin

Human gene fragmen Human endostatin c SEQ ID 50 of WO991 Nucleotide sequenc Specific tumour ce Reproductive recom Anticancer gene-as Alternate human en Human gene fragmen Nucleotide sequenc

Human endostatin c Mouse endostatin c

Endostatin coding Murine endostatin

AAZ50398 AAX84635 AAX79949

ABK09978

Synthetic plasmid

endostatin c Human endostatin e

AAX77720 ABQ81193 AAH79104 AAL55454 AAL44000

ABQ76079

Human ovarian anti Human collagen 18 Human endostatin ( Rat endostatin enc Rat endostatin enc DNA encoding anti-

ALIGNMENTS

AAX58740

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Mouse

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Human endostatin D
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Human angiogenesis
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7009.423 Million cell updates/sec
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              GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; plaque neovascularisation; coronary collateral; artiovenous malformation; cerebral collateral; arteriovenous malformation; eschaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiathritic; antipsoriatic; antidiabetic; ophthalmological;
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AAL46063 standard; cDNA; 555 BP
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Best Local Similarity
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                                                                                                              The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque meovascularisation, telanglactasia, haemophiliac joints, angiotibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, isohaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGGCTGGCCGCACCTTCCGGGCCTTCCTGTCGTCGCGCCTGCAGAGACCTCTACAGAGACTC 180
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                                                                                                                                                                                                                             angiogenesis-related disorder, such as cancers or diabetic retinopathy,
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                                                                                                                                                                                                                isolated nucleic acid molecule for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 555 BP; 78 A; 203 C; 191 G; 83 T; 0 other;
                                                                                                                                                                                                                                                  encodes an endostatin protein -
                                                                                                                                                                                                                                                                                  Claim 2; Fig 4; 56pp; English
                                                            25-AUG-2000; 2000US-227924P.
                             24-AUG-2001; 2001EP-0307224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endostatin coding sequence.
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Matches 555; Conservative
                                                                                             (PFIZ ) PFIZER PROD INC
                                                                                                                                Tong X;
                                                                                                                                                               WPI; 2002-354068/39.
                                                                                                                                                                                P-PSDB; AAO17430
                                                                                                                              Sheppard MG,
27-MAR-2002
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The present invention provides the protein and coding sequences of canine pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, rheumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, cornary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; cerebral collateral; arteriovenous malformation; cerebral collateral; diabetic neovascularisation; fracture; cytostatic; antiathritic; antipsoriatic; antidiabetic; ophthalmological;
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corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pro-endostatin; endostatin; angiogenesis; cancer; gene therapy;
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/product= "pro-endostatin"
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98US-0097883

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(LEXI-) LEXINGEN PHARM CORP.

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                                                                    259 GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC
                                                                                                                                       GTGCGCCGCCGACCGCACCGGGTCCTCTAACCTCAGGGACGACGACGCTCTTC
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The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that mays be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, theumatoid arthritis, psoriasis, ocular angiogenic diseases c. g. diabetic retinopathy, retinopathy of prematurity, macular celegeneration, corneal graft rejection, neovascular glaucoma, retrolental collibroplasia, rubboois and osler-Webber syndrome; mycocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encoding canine conduction, integrin used in the construction of immunofusin containing canine
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Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -
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01-NOV-1999;

Score 419.6; DB 24; Length 1564; Pred. No. 1.7e-62;

75.6%; 84.8%;

Query Match Best Local Similarity

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vascular endothelial cytopoiesis inhibiting factor; inhibitor;
fusion construct; ds.
                                                              GAGGCCCCGGCGCCACCGGGCAGGCGTCGTCGCTGCTGCGGGGCAGGCTGCTGCTGCTGCTGGCAGGAGCAG
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/transl except= (pos58..60,aa:Ala)
/transl_except= (pos:811..816,aa:GGGGSGG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding human Endostatin/IgG1Fc fusion construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiofibroma and wound granulation, for treatment of diseases related to excessive or abnormal stimulation of endothelial cells e.g. intestinal adhesions, atherosclerosis, scleroderma. The protein may also be useful as a birth control agent by reducing or preventing uterine as a birth control agent for endostatin may be isolated from cells or tissue that express high levels of endostatin, eg. tumour cells, by generating cDNA from mRNA using reverse transcriptase and then amplifying
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                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes an endostatin protein which is the carboxy terminal protein of human collagen XVII. Recombinant mouse endostatin (20 mg/kg) was administered subcutaneously to mice implanted with Lewis lung carcinomas. There was tumour mass regression non-detectable levels after 12 days of therapy due to the angiogenesis inhibitory activity of endostatin. Thus the protein is useful for treatment of angiogenesis-dependent cancers. The polymucleotide and polypeptide sequences of this endostatin are useful for treating and diagnosis of tumours, ocular angiogenic diseases. Osler-Webber syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints,
                                                                                                                                                                                                                                                                       Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers and as birth control agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CACACCCACCAGGACTTCCAGCTGGTGCTGCTGGTGGCCCTGAACAGCCCGCAGCCG
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Pred. No. 3.4e-62;
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                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 39; 68pp; English
                                                                                              (CHIL-) CHILDRENS MEDICAL CENT,
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85.3%;
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99US-0315689
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                                                                                                                                                                                                WPI; 2000-365617/31.
P-PSDB; AAY94323.
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Best Local Similarity
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                                                                                                                                              O'Reilly MS,
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481 GAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC 540
                                      481 AGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATTGAGAACAGCTTCATGACT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine angiostatin, human or murine endostatin and angiogenesis-inhibiting fusions and fragaments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasminogen; human; angiostatin; endostatin; gene therapy; vector; anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel viral gene therapy vector comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CACACCCACCAGGACTTCCAGCTGGTGCTGCTGGTGGCCCTGAACAGCCGCAGCCG
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85.3%; Pred. No. 3.4e-62;
Live 0; Mismatches 80
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(MASI ) MASSACHUSETTS INST TECHNOLOGY.
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abnormal-vessel diseases. The IAF antibody is preferably a polyclonal antibody, mosaic antibody, single stranded antibody and human originated antibody.
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                                                                                                                                                 80; Indels
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                                                                             Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
                                                                                                            Score 418; DB 21;
Pred. No. 3.4e-62;
0; Mismatches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiogenesis inhibiting factor 1 and its derivative useful for treating tumors -
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                                CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCCAGCTGAAGCCCGGGGCCCGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis inhibiting factor 1; IAF-1; tumour; antibody;
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product= "Endostatin(TM) C-terminus minus 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   having angiostatin activity, a collegen XVIII fragment having endostatin activity, a collegen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used too inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours tumour metastasis, benign tumours including tumours, reachemas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis and osler Webber syndrome; mycoardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in the present sequence is a CDNA encoding human electric in gene therapy. The present sequence is a CDNA encoding human electric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCTGGCGGCCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of plasminogen fragment, however, the rest of the specification refers to this sequence as being nucleotide sequence of human endostatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel fusion protein of angiostatin or endostatin and an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin gamma (IgG) Fc fragment.
Note: This sequence is stated in claim 12 as being amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                 /product= "Endostatin"
/note= "Does not include stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Pages 40-41; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTCCTTTGACGCCAAGGACGTCCTGAGGCACCCCACCTGGCCCCCAGAAGAGCGTGTGG
                                                                                                                                                                                                                                                                     361 CATGGCTCGGACCCCAACGGGCGCAGGCTGACCGAGAGCTACTGTGAGACGTGGCGGACG
                                                                     TTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGGCCTGGCCCCGGAAGAGCGTGTGG
                                                                                                                                                                                                   CACGGCTCCGACCCCAGCGGCGCCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACG
                                                                                                                                                                                                                                                                                                                                                                                                         421 GAGGCTCCCTCGGCCACGGCCCAGGCCTCCTCGCTGCTGGGGGCCAGGCTCCTGGGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene; human; plasminogen; angiostatin; neovascularisation;
kringle domain; cell proliferation; viral vector;
replication-defective; cancer; tumour; ss.
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haemangioma, acoustic neuromas, neurofibromas, trachomas, and pyogenic

granulomas, rheumatoid arthritis, psoriasis, coular angiogenic diseases,
e.g., diabetic retinopathy, retinopathy of prematurity, macular

degeneration, corneal graft rejection, neovascular glaucoma, colon

cancer, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome,
myocardial angiogenesis, plaque neovascularisation, telangiectasia,
haemophiliac joints, angiofibroma, and wound granulation. Endostatin(TM)
is also useful for treating disease of excessive or abnormal stimulation
of endothelial cells such as intestinal adhesions, atherosclerosis,
scleroderma and hypertrophic scars. Higher yields of more purified, and
biologically active Endostatin(TM) are obtained by the new method.
C Endostatin(TM) can be stored in buffers for extended periods of time, and
also subjected to lyophilisation, while preserving biological activity.
C Centrifugation of broth from fermentation steps in production is avoided,
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      /note= "None of the above CDSs have start or stop codons"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention is useful for producing, recovering and purifying Endostatin (TM) from biological sources, such as biological fluids, tissues, cells, culture media, and fermentation media. Endostatin(TM) is useful for treating angiogenesis mediated diseases such as solid tumours, blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preventing unwanted potential cellular lysis and contamination with additional proteins, pigments, enzymes and other cellular chemicals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumours, comprises recombinantly producing the protein using an expression system, and recovering and purifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boerner RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encodes Human Endostatin(TM). The new method of the
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y FR, Shepard SR, Schrimsher JL;
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P-PSDB; AAU00896, AAU00897, AAU00899.
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llarity 85.3%; Pred. No. 3.4e-62;
Conservative 0; Mismatches 80
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                                                                                                                                                                                                          14-SEP-2000; 2000WO-US25166
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         of
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         Note: This sequence is given incorrectly in the sequence listing
the specification as an amino acid sequence.
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                                                                    80; Indels
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                                  Seguence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
                                                   ; DB 25;
3.4e-62;
                                                  Score 418; DB; Pred. No. 3.4e-0; Mismatches
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Matches 466, Conservative
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The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the proteins can be used for inhibiting the proteins calls (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor. Growth. The present sequence is used in the course of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Streptomyces. Leader sequences of Streptomyces sp. strain CS SnpA and S. venezuelae alpha-amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer, inhibition of tumour growth, inhibition of angiogenesis, isolation of receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced.
                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of human endostatin encoded by plasmid pMALcH#15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of soluble recombinant endostatin involves transforming Streptomycete host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader
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the DNA sequences encoding them. Angiogenesis is the generation of new blood vessels into a tissue, and normally occurs in wound healing, foetal and embryonal development and the formation of the corpus luteum, endometrium and placenta. Angiostatin is a protein (see AAB16450 and AAA68202) involved in angiogenesis, and has an amino acid sequence similar to that of a plasminogen fragment (see murine plasminogen AAB16490). Angiostatin has the ability to inhibit angiogenesis. Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and AAA68203). Sequences AAA68242 and AAB16452 represent coding and protein sequences of human laminin. Laminin is an angiostatin binding protein, and some of the peptides of the invention share homology with regions of laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the angiogenesis-inhibiting protein receptor fragments of the invention. The peptides had an angiostatin and can be used in methods the angiostatin or endostatin and can be used in methods
                                                                                                                  This invention relates to angiogenesis-inhibiting protein receptors, and
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Disclosure; Page 86; 100pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancers, inflammation, rheumation arthritis, chronic articular rheumatism, psoriasis, disorders associated with inopportune invasion of prematurity, macular degeneration, corneal graft rejection, retrolental fibroplasia, rubocsis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent alseases include osler-webber syndrome, mycardial angiogenesis, plaque neovasculisation, telangiectasia, haemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GGGCTGGCGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC
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                                                                                                                                                    chicken;
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                                                                                                                                                  Endostatin; antiangiogenic; angiogenesis; human; mouse; cancer; inflammation; angiogenesis-dependent disease; de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;
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Pred. No. 3.4e-62
                                                                                                                  Human endostatin coding sequence SEQ ID NO: 1.
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              AAC88289 standard; DNA; 552
                                                                                                                                                                                                                                                                                                           02-MAY-2000; 2000WO-US12063
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy
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P-PSDB; AAB49379.
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                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human; angiogenesis; PITSLRE protein kinase; cancer; arthritis; macular degeneration; diabetic retinopathy; angiogenic-related disease; haemangioma; blood borne tumour; leukaemia; neovascularisation; coronary collateral; cerebral collateral; neovascular glaucoma; corneal disease; wound healing; Helicobacter related disease; keloid; ovulation; menstruation; gene; ss.
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                     human endostatin.
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c a composition comprising a protein that is homologous to PITSIRE

protein kinases (PK) and an angiogenic factor. The method is useful

for regulating angiogenesis related to cancer, arthritis, macular

degeneration, and diabetic retinopathy. The compositions are useful

for inhibiting angiogenic-related diseases. The method and

compositions are useful in treating diseases and processes that are

mediated by angiogenesis including haemangioma, solid tumours, blood

borne tumours, leukaemia, metastasis, telangiectasia, psoriasis,

corner typogenic granuloma, myocardial angiogenesis, Crobn's

clisease, plaque neovascularisation, coronary collaterals, cerebral

collaterals, arteriovenous malformations, ischaemic limb angiogenesis,

corneal diseases, rubeosis, neovascular glaucoma, diabetic retinopathy,

retrolental fibroplasia, arthritis, neovascular glaucoma, diabetic retinopathy,

retrolental fibroplasia, arthritis, pebtic ulcer, Helicobacter related

diseases, fractures, keloids, vasculogenesis, haematopoiesis,

menstruation, placentation, and cat scratch fever. The minimal side

the invention provides a therapy for cancer that has minimal side

custored the present sequence encodes human endostatin which is
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Search completed: August 17, 2003, 13:19:26 Job time : 214.739 secs

The present invention relates to methods and compositions of inhibiting angiogenesis. The method comprises administering to a human or animal

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Sequence 4, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 37, Appli
Sequence 12, Appli
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Sequence 1103, Appli
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Sequence 30, Application US/09206059

Patent No. 6201104

Patent No. 6201104

APPLICANT: MacDonald, Nicholas

APPLICANT: Sim, Kim Lee

TITLE OF INVENTION: Proteins and Methods of Use

TITLE OF INVENTION: Proteins and Methods of Use

TITLE OF INVENTION: Proteins and Methods of Use

CURRENT APPLICATION UNMER: US/09/206,059

CURRENT FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 30

LENGTH: 552
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Pred. No. 8.3e-74;
0; Mismatches 80; Indels
Sequence 4, Application US/08159784

Fatent No. 5643783

GENERAL INFORMATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREE: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                               COUNTR: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1,1993
CLASSIFICATION: 530
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REFERENCE/DOCKET NUMBER: 00)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-6970
TELEFAX: (617) 542-8906
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al Similarity 85.3%;
466; Conservative (
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ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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STRANDEDNESS: single
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GGGCTGGCCGGCACCTTCCCGGGCCTTCCTGTCGCGGCTGCAGGACCTCTACAGCATC 180
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                                                                                                                                           Sequence 3, Application US/09449293
; Sequence 3, Application US/09449293
; Patent No. 6267954
; GENERAL INFORMATION:
; APPLICANT: Abitbol, Marc
; APPLICANT: Menasche, Maurice
; APPLICANT: Bonnel, Sebartien
; APPLICANT: Bonnel, Sebastien
; APPLICANT: Pates, Herve
; APPLICANT: Neuner-Johne, Martin
; APPLICANT: Neuner-Johne, Martin
; APPLICANT: Neuner-Johne, Martin
; TILLE REFERENCE: 8076.2020501
; CURRENT APPLICATION NUMBER: US/09/449,293
; CURRENT FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NOS: 3
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1 CACACCCACCAGGACTTCCAGCTGGTGCACCTGGTGGCCCTGAACAGCCCGCAGCCG
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Pred. No. 1.4e-65;
0; Mismatches 112;
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Best Local Similarity 79.8%;
Matches 443; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Rattus rattus
US-09-449-293-3
                                                                                                                                      RESULT 5
US-09-449-293-3
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                         CATGGCTCGGACCCCAACGGGCGCAGAGCTGACCGAGAGCTACTGTGAGACGTGGCGGACG
                                                                                                                                                            1 GACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCAGGCGCCATGCGG
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        TTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGG
                                                                        CACGGCTCCGACCCCAGCGGCGCCCTGACCGACAGCTACTGCGAGACGTGGCGGACG
                                                                                                                                         GAGGCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGGCGGGCAGGCTGCTGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Folkman, Judah
APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 534
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Pred. No. 1.9e-72;
0; Mismatches 77; Indels 0
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Patent No. 6346510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                       2044 GĊĊŢCC 2049
                                                                                                                                                                                                                                                                        541 TCCTTC 546
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          US-09-315-689-6
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APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 GGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGCTTCCAGCAAGCCCGAGCCGTG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE:
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Pred. No. 1.4e-65;
0; Mismatches 112;
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                                                                                                                                                                                                                                                   ; Sequence 37, Application US/08985526
; Patent No. 6080728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: McMorrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
TELEFAX: (302) 658-5613
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                                                                                       544 rcrrrcrccaarag 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 565 base pairs
TYPE: nucleic acid
                                541 TCCTTCTCCAAGTAG
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-985-526-37
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Matches 443; Conserv
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                         RESULT 7
US-08-985-526-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 GGGCTGTCGGGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 GTGCGCCGTGCTGACCGGGGGTCTGTGCCCATCGTCAACCTGAAGGACGAGGTGCTATCT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rrrrrrrakceckedadarercergadacaccecadecececkeadadadegrared 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 AAAGCTGCGAGACCACAACAGCTACATCGTCCTGTGCATTGAGAATAGCTTCATGACC 543
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APPLICANT: Wan Den Berghe, Loic
APPLICANT: Bonnel, Sebastian
APPLICANT: Berte, Herve
APPLICANT: Herve
APPLICANT: Neuner-Jehle, Martin
APPLICANT: Neuner-Jehle, Martin
APPLICANT: Neuner-Jehle, Martin
APPLICANT: Neuner-Jehle, Martin
FILE REPERENCE: 8076.2020182
CURRENT APPLICATION NUMBER: US/09/775,325
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: US/09/449,293
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                                                                                                                                                                                                                                                   Sequence 3, Application US/09775325 Patent No. 6500449
                                                                                                                                                                                                                                                                                                                                                                                                      Menasche, Maurice
Bossard, Carine
Van Den Berghe, Loic
Bonnel, Sebastian
Prats, Herve
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Best Local Similarity 79.8%;
Matches 443; Conservative (
                                   541 TCCTTCTCCAAGTAG 555
                                                                              544 TCTTTCTCCAAATAG 558
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                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Abitbol, Marc
APPLICANT: Uteza, Yves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Rattus rattus
US-09-775-325-3
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LENGTH: 558
                                                                                                                                                                                         RESULT 6
US-09-775-325-3
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APPLICANT:
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3433 GGGCTGTCGGGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATC 3492
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APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
PILE REPERENCE: 4001.002500
CURRENT APPLICATION NUMBER: US/09/561,500
CURRENT APPLICATION NUMBER: 06/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: DESCRIPTION
OTHER INFORMATION: OLIGONUCLEOTIDE
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Pred. No. 4.1e-65;
0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 12, Application US/09561500; Patent No. 6342219; GENERAL INFORMATION:
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Best Local Similarity 79.9%;
Matches 440; Conservative (
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; LOCATION: (1)..(573)
US-09-561-500-12
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Patent No. 5643783
GENERAL INFORTION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
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MEDIUM TYPE: 3.5. Diskette, 1.44 Mb
COMPUTER: 128 Diskette, 1.44 Mb
CO
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REFERENCE/DOCKET NUMBER: 00246/170001
TELECOMMUNICATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4031
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US-08-159-784-1
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Sequence 12, Application US/09561526

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Sequence 12, Application US/0961526

Septicant No. 6416758

TITLE OF INVENTION: ANTHEORY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF

TITLE OF INVENTION: ANTHEORY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF

FILE REFERENCE: 4001.002586

CURRENT APPLICATION NUMBER: US/09/561,526

CURRENT APPLICATION NUMBER: 00/131,432

PRIOR APPLICATION NUMBER: 00/131,432

PRIOR PLING DATE: 1999-04-28

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 12

LENGTH: 573

TYPE: DAA

ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

OTHER INFORMATION: OLIGONUCLEOTIDE

NAME/KEY: CDS

LOCATION: (1) ..(573)

US-09-561-526-12
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79.9%; Pred. No. 4.1e-65;
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APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIHODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: US/09/561,108
CURRENT FILING DATE: 2000-04-28
PRIOR PRILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 373.4; DB 4; Length
Pred. No. 4.1e-65;
0; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09561108; Patent No. 6342221; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 79.9
Matches 440; Conservative
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, LOCATION: (1)..(573)
US-09-561-108-12
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US-09-561-108-12
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LENGTH: 573
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GENERAL INCORNATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AEUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 2102
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                                                                 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC 300
                                                                                                                                                                                                                                                                                                                CACGGCTCCGACCCCAGCGGCGCCGCCTGACCGACAGCTACTGCGAGACGTGGCGGACG 420
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   202 GTGCGCCGTGCTGACCGGGGGTCTGTGCCCATCGTCAACCTGAAGGACGAGGTGCTATCT 261
                                                                                                                            CCCAGCTGGGACTCCCTGTTTTCTGGCTCCCAGGGTCAACTGCAACCCGGGGCCCGCATC 321
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Pred. No. 0.00066; '
0; Mismatches 202; Indels
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 48.8
Matches 195; Conservative
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US-09-252-991A-2102
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Patent No. 6524583

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Breaken
TITLE OF INVENTION: ANTHRODY WETHODS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002582
CURRENT APPLICATION NUMBER: US/09/561,499
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 573
                                                                                                                                                                                                                                                                                                TTTTCTTTTGACGCAGAGATGTCCTGAGACACCCCAGCCTGGCCGCAGAAGAGAGATGTTGG
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                                                                                                                                                                      CCCAGCTGGGACTCCCTGTTTTCTGGCTCCAGGGTCAACTGCAACCCGGGGCCCGCATC
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CTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
CTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
LOCATION: (1)..(573)
US-09-561-499-12
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                                                                                                                                                                                                                     Sequence 1793, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.1131 US/09/252,991A
CURRENT RPELICATION NUMBER: US/09/252,991A
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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Pred. No. 0.00066;
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PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
1 DAVAN. 1793
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8.09-252-991A-1861/c
; Sequence 1861, Application US/09252991A
; Patent No. 6551795
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Best Local Similarity 48.8
Matches 195; Conservative
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Pred. No. 0.0012;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Job time : 60.5426 secs
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Best Local Similarity 50.4%;
Matches 172; Conservative
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TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as TITLE OF INVENTION: Immunofusins ETHER REPERBRICE: LEX-006C1 CURRENT APPLICATION NUMBER: US/10/292,418 CURRENT APPLICATION NUMBER: US/10/292,418 CURRENT FILING DATE: 2002-11-12 PRIOR APPLICATION NUMBER: 09/383,315 PRIOR APPLICATION NUMBER: 09/383,315 PRIOR APPLICATION NUMBER: US 60/097,883 PRIOR FILING DATE: 1998-08-25 NUMBER OF SEQ ID NOS: 54 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 34 LENGTH: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS

LOCATION: (1)..(552)

OTHER INFORMATION: Endostatin

US-10-292-418-34
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5967.841 Million cell updates/sec
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1. / cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
1. / cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
1. / cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
1. / cgn2_6/ptodata/2/pubpna/PCTUG_PUBCOMB.seq:*
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1. / cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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1. / cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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δ	Description	418-34 Sequence 34, Appl	Sequence 5		Sequence 3	Sequence 53	0,	107-2178 Seguence 2178, Ap				Sequence 6,	Sequence 59,		Sequence 3, 1	0,	Let 0.00
SUMMARIES	ID	US-10-292-418-34	US-10-131-241-50	US-10-042-	US-10-292-418-3	US-10-131-	US-09-873-6	-088-60-SD	US-10-060-	US-10-080-	US-10-131-	US-10-042-347-6	US-10-131-	US-10-131-	US-09-775-1	US-09-775-325-3	20 000 000 01
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1 CACACCCACCAGGACTTCCAGCTGGTGCTGCTGGTGGCCCTGAACAGCCCGCAGCCG

Query Match

99.2%; Score 550.4; DB 12; Length 552;
Best Local Similarity 99.8%; Pred. No. 7.7e-117;
Matches 551; Conservative 0; Mismatches 1; Indels 0;

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17		67.4	624	13	US-10-080-797-4	Sequence 4, Appli
18		67.3	573	10	US-09-998-831-12	12,
19		67.0	552	12	0 - 292 - 418 - 1	17,
20	187.8			14	-036	
21	171.2	30.8		12	US-09-971-392-159	159,
20	95.4			14	118-10-131-241-45	45
23	74.4			14	US-10-060-036-4	4
24	58.4			-	US-10-156-761-4493	
25	58.4	10.5	90		92-9	Sequence 1, Appli
. 26	57			Ч	US-10-156-761-3078	Seguence 3078, Ap
c 27	57		96	14	US-10-156-761-1	Sequence 1, Appli
28	9			14	US-10-076-816-3	Sequence 3, Appli
29	56.2			14	US-10-077-381-3	
30				14	US-10-156-761-7479	
31	S			14	US-10-156-761-3274	,
32	55.6			14	US-10-156-761-3928	(-)
33	4			14	US-10-156-761-5404	٠,
34					US-10-148-907A-14	•
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36	53.6			14	US-10-304-928-13	Sequence 13, Appl
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c 39	3		ω		US-09-976-059-1	ı,
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GENE	GENERAL INFORMATION:	MATION				
; APPI	APPLICANT: Lo	o, Kin	Kin-Ming			
; APPI		Li, Yue				
, APP1	APPLICANT:	Gillies,	s, Stephen D	en D		

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us-lucuace 4, Application US/10042347

publication No. US20030114370A1

GRNERAL INPORMATION:

APPLICANT: O'Reilly, Michael S.

APPLICANT: C'Reilly, Michael S.

APPLICANT: C'INCHINION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide Frairing C INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide Frairing Price Or INVENTION: Thereof

FILE REFERENCE: 05213-0880 (43170-249874)

CURRENT FILING DATE: 1090-01-11

PRIOR FILING DATE: 1099-10-30

PRIOR FILING DATE: 1999-0-16

PRIOR FILING DATE: 1996-10-20

PRIOR FILING DATE: 1996-00-16

PRIOR FILING DATE: 1996-00-16

PRIOR FILING DATE: 1996-00-16

PRIOR FILING DATE: 1996-00-17

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 546
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                                                                                                                                                    241 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC
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Pred. No. 1.2e-86;
O; Mismatches 80;
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85.3%;
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Best Local Similarity 85.3°
Matches 466; Conservative
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APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer, TITLE OF INVENTION: Compositions and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 50
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Pred. No. 7.7e-117;
0; Mismatches 1;
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Matches 551; Conservative
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ORGANISM: Canine sp
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Gaps

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APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer:
TITLE OF INVENTION: Compositions and Regulating Angiogenesis Using Cancer Markers
FILE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
CURRENT PELLING DATE: 2002-07-22
FRIOR APPLICATION NUMBER: US 09/413,049
FRIOR FILING DATE: 1999-10-06
FRIOR FILING DATE: 1999-10-06
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Version 3.1
SEQ ID NO 53
FRIOR FILING DATE: 549
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Pred. No. 1.2e-86;
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; Sequence 53, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-131-241-53
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Publication No. US20030139365A1
GENERAL INFORMATION:
APPLICANT: Lo, Kin-Ming
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Li, Yue
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION INMER: US/10/292,418
CURRENT FILING DATE: 1999-08-25
PRIOR PELLING DATE: 1999-08-25
PRIOR PELLING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PALENTIN VOY: 2.0
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Pred. No. 1.2e-86;
0; Mismatches 80;
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OTHER INFORMATION: endostatin
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Best Local Similarity 85.3
Matches 466; Conservative
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Patent No. US20020142981A1

SEQUENCE LINFORMATION:

APPLICANT: HORNEY LOSE

APPLICANT: Correct T.

APPLICANT: Genetic US.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

CURRENT FILING DATE: 2001-06-14

PRIOR PAPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR PILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver: 2.1

LENGTH 3344
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US-09-880-107-2178
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ORGANISM: Homo sapiens
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                               CCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGGCACGCATC 300
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Pred. No. 1.2e-86;
0; Mismatches 80;
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Best Local Similarity 85.3%;
Matches 466; Conservative
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ORGANISM: Homo sapiens
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US-09-873-676-30
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GTGCGCCGTGCCGGCGCGCGCGCGCGTCGTCGAACCTCAAGGACGAGCGGCTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Campochiaro, Peter A.
APPLICANT: Dixon, Katharine H.
APPLICANT: Brazzell, Romulus K.
TITLE OF INVENTION: METHOD FOR TREATING OCULAR
TITLE OF INVENTION: NEOVASCULARIZATION
FILE REPERBNCE: 4-31881A
CURRENT APPLICATION NUMBER: US/10/080,797
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 21
SOFTWARE FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/10080797; Publication No. US20020183253A1; GENERAL INFORMATION:
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; ORGANISM: Human
US-10-080-797-2
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                                                                  GTGCGCCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC
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APPLICANT: Kalos, Michael D.
APPLICANT: Lodge, Michael J.
APPLICANT: Lodge, Michael J.
APPLICANT: Dereing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FRSESE FOR Windows Version 4.0
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Pred. No. 8.8e-87;
0; Mismatches 80;
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Best Local Similarity 85.33
Matches 466; Conservative
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ORGANISM: Homo sapiens
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361 Db 360 Qy 421 Db 420 Qy 481 Db 540 Qy 541 Db Cell Prolifer 7 7 6	PRIOR PRIOR NUMBER	60 ; SEQ ID NO 6 5 LENGTH: 5 60 ; TYPE: DNA 7 120	120 Ouery Matc 120 Query Matc 160 Matches 4 180 Qy 1	160 Db 1	220 Db . Qy 1 280 Db . 1
Operation	74.9%; Score 415.6; DB 14; Length 632; Similarity 82.8%; Pred. No. 4.1e-86; 3; Conservative 0; Mismatches 29; Indels 80;	1 CACACCCACCAGGACTTCCAGCTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCG	121 GGGCTGCGGCACCTTCCGGGCTTCCTGCGCGCGCGCGCGC	161	161 IGCAGGACCTCTACAGCATCGTGCCGCGCGACCGCACCGGGGTGCCGTCGTCACCTACTTCACCTACCT

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APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifere
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifere
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REPERRICE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR PILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 540
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241 GCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCACGCATCTTCTCCTTTGAC 300
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Pred. No. 3.1e-83;
0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-10-131-241-48
; Sequence 48, Application US/10131241
; Publication No. US20030012792A1
; GENERAL INFORMATION:
; APPLICANT: Holaday, John W.
; APPLICANT: Fortier, Anne H.
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Best Local Similarity 84.2%;
Matches 454; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Rhesus monkey
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US-10-131-241-59
US-10-131-241-59
Sequence 59, Application US/10131241
Publication No. US20030012792A1
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Fortlar, Annu H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILIE REPRENCE: 05213-034; 43170-271565
CURRENT APPLICATION NUMBER: US 105/0/131,241
CURRENT FILING DATE: 1999-10-06
FRIOR APLICATION NUMBER: US 09/316,802
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
COFTWARE: PatentIn version 3.1
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                                                                         GCCTTAITCTCGGGCTCCGAGGCCAGCTGAAGCCCGGGGCCCGCATCTTCTTTCGAC 312
                                                                                              GGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGGCACGGCTCCGAC 372
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 GACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTCCCCCAGCTGGGAG
                       GACCGCAGCCGTGCCCATCGTCAACTCAAGGACGAGCTGCTGTTTCCCAGCTGGGAG
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151   CACCOTCONACCOCOACCCTACACCACACACACACACACACACACACAC	QY         421 GAGGCCCGGGGGGGCAGGCGTCGTCGCGGGGGGGGGGGG	RESULT 15  US-09-775-325-3  Sequence 3, Application US/09775325  Fatent No. US20020076397A1  GENERAL INFORMATION:  APPLICANT: Abitbol, Marc  APPLICANT: Menasche, Mauxice  APPLICANT: Bonnel, Sebastian  APPLICANT: Bonnel, Sebastian  APPLICANT: Bonnel, Sebastian  APPLICANT: Prats, Horve  APPLICANT: Prats, Horve  APPLICANT: Prats, Horve  APPLICANT: Prats, Horve  APPLICANT: Prats, Wartin  APPLICANT: Neuner-Jehle, Martin  APPLICANT: 100-20201  PRIOR APPLICATION NUMBER: US/09/775,325  CURRENT APPLICATION NUMBER: US 09/449,293  PRIOR APPLICATION NUMBER: US 09/449,293  PRIOR PILING DATE: 1999-11-24  NUMBER OF SEQ ID NOS: 5  SEQ ID NO 3  LENGTH: 558  TYPE: DNA  CRAMISM: Rattus rattus  US-09-775-325-3	Query Match 67.7%; Score 375.8; DB 9; Length 558; Best Local Similarity 79.8%; Pred. No. 5e-77; Matches 443; Conservative 0; Mismatches 112; Indels 0; Gaps 0;	Oy 1 CACACCACGAGACTTCCAGGTGTGCTGCTGGTGGTCGCCTGAACAGCCGCAGCCG 60	Qy         61         GCGGCATGCGAGCATCCGGGAACGCACTTCCAGTGCTTCCAGCAGGCGCGCGC	QY         121 GGGCTGGCCGGCCCTTCCGGGCCTTCCTGTCGCGCCTGCAGGACCTCTACAGCATC 180	Oy 181 GTGCGCGCGCGCAACAGCGGGGTGCCCGTCAACCTCAAGGACGAGGTGCTCTTC 240	Oy 241 CCCAGTGGGAGGCCTTATTCTCGGGCTCCGAGGCCAGCTGAAGCCCGGGGCCCGCATC 300 [	QY 301 TTCTCTTTCGACGCAGAGATGTCCTCCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGG 360	. Oy 361 CACGGCTCCGACCCCAGGGGGCGCCGACCGACAGCTACTGCGAGACGTGGCGGACG 420
- 10 10 90 90 90 90 90 - 57 (BETTERFORDING MAINE NAME OF A MAIN TO A M	GGACG       GGACA AGCAG       GGCAG TGAC 5	4 RANSPLANTATION OF ENCAPSULATED CE 7775,174 49,293	Similarity 79.8%; Score 375.8; DB 9; Length 558; Similarity 79.8%; Pred. No. 5e-77; 3; Conservative 0; Mismatches 112; Indels 0; Gaps			GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGCGCGCTGCAGGACCTCTACAGCATC	GIGCGCCGCGCCGCACCGGGGGGCCCGTCAACCTCAAGGACGAGGTGCTCTTC	CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCAGCTGAAGCCCGGGGCCCGCATC	TTCTCTTTCGACGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGG	CACGCTCCGACCCCAGCGGCGCCCGACACAGCTACTGCGAGACGTGGCGGACG 

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ζŏ	481 GAGGCGGGAGCTGCGCCACGC	481 GAGGCGCGAGCTGCCGCCACCCTTCGTGGTCCTCGAGAACAGCGTCATGACC 540	540

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Search completed: August 17, 2003, 16:34:30 Job time: 218.125 secs

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CR44165 695295 MA
B0615520 UI-H-FG0B0672290 AGENCURT
BM883067 UI-H-FG0BM883067 UI-H-FG0B1412588 60296468
B1412588 60296468
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B181080524 602454749
B0673186 AGENCOURT
B1080524 602877005
AN911243 MG3H10.9
B161007 602865213
B072324 AGENCOURT
B1247582 60296041
B1247582 60296041
B125329 AUS12514
B125391 MM125614
B155613 AUS12514
B155613 AUS12514
B155613 AUS12516
B115566 6031586
B115566 60352782
AUS5613 AUS1611
B117444 602914008
B1155613 601775586
B1155613 601775586
B115556 60352782
AUS5612 AUS1611.2
AUS5613 AUS1611
B1196935 603176586
B115596 60352782
AUS98137 UI-H-DT1B11998137 UI-H-DT1B1195935 603167356
CR601615 AGENCOURT

OM nucleic

Run on:

Searched:

Database

Sequence:

Perfect

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1 (bases 1 to 551)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casa,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF074459 551 bp mRNA linear 221883 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                        BI147444
BF166139
BU352506
AI858615
BM998137
BU45935
BQ772348
AA288198
AM192502
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AI970297
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BG387051
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BI161007
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BI904605
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BU632049
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 Keele, J.W.
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RESULT 1
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DEFINITION
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COMMENT
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BE908201 601500458
BE906253 601502237
CD105862 AGENCOURT
                                                                                                               (without alignments)
8338.472 Million cell updates/sec
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                                                                                               August 17, 2003, 13:19:37 ; Search time 1617.68 Seconds
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              GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                     22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                                                              lotal number of hits satisfying chosen parameters:
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Listing first 45 summaries
                                                                    nucleic search, using sw model
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AW243446 xm95d11.x BF178591 601807962 BU158380 AGENCOURT CB454313 598557 MA BQ567187 gi80h10.y

A1970297 wr09c02.x BU439577 603208252

EST 25-APR-2001

Score

Result No. 0 m 4

score g Pred.

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NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMP704 row: d column: 16
High quality sequence stop: 688.
Location/Qualifiers
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 707)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3902175"
                                                                                                                                         Unpublished
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                sapiens (human)
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BE908201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CTGCCCGTCGTCAACCTCAGGGACGAGGTGCTGTTTCCTAGCTGGAGGCCTTGTTCTCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 GCCTCCTCGCTGGTGGCGGGCCGGCTGCTGGAGCAGAAAGCCGCCGGGTGCCACAACGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 GCGGACTTCCAGTGCTTCCAGCAGGCGCGCGCGGGGGCTGGCCGGCACCTTCCGGGCC 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTCCCCAGCTGGGAGGCCTTATTCTCG 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                /clone lib= MARC 2BOV"
/clone=lib= MARC 2BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, thymus,
semitendonous muscle, longissimus muscle, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATCTTCTTTTCGACGCAGAGATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCTGACCGACAGCTACTGCGAGACGTGGCGGACGGAGGCCCCGGCGGCCACCGGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.2%; Score 439.8; DB 10; Length 551; 89.3%; Pred. No. 3.4e-72; ive 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                 adrenæl, and endometrium.
200 c 179 q 92
                                                                                                     FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCAGGACG
Plate: 81 row: F column: 9
seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                   /organism="Bos taurus"
                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                179 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.2
Best Local Similarity 89.3
Matches 474; Conservative
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/tissue_type="epithelioid carcinoma"
/tab host="DH10B (phage-resistant)"
/clone_lib="NHH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Sete_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Technologies."
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85.3%; Pred. No. 3.8e-68;
ive 0; Mismatches 80;
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BE908201.1 GI:10402537

DEFINITION

ACCESSION VERSION

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/clone="IMAGE:3055831"
/tissue_type="Pituitary"
/tissue_type="Pituitary"
/tish_bost="DHI0B-Ton A ( T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: ECORV
(destroyed); Site_2: Not1; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon cloning
). Average insert size 1.1 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 15-MAY-2003
276 CCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCCGGGGCACGCATC 335
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1 (Dases 1 to 881)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                336 TTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCACCTGGCCCCCAGAAGAGGCGTGTGG
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                                             TTCTCTTTCGACGGCAGAATGTCCTGCAGCACCCCGCCTGGCCCCGGGAAGAGCGTGTGG
                                                                                                                              CACGGCTCCGACCCCAGCGGCGCCCTGACCGACAGCTACTGCGAGACGTGGCGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
Plate: NDAM424 row: g column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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AGENCOURT 14021788 NIH MGC_179 Homo sapiens cDNA clone
IMAGE:30355831 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 3.9e-68;
0; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 689
Location/Qualifiers
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85.3%;
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Homo sapiens
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/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH10B (phage-resistant)"
/note="Organ: pancreas: Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1:1 kb. Library constructed by Life
Technologies."
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                                                                                                                                                                                                                     BE906253 3 757 bp mRNA linear EST 20-OCT-2000 001502237F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3904208 5',
                         550
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.lln.gov
Plate: LLAM9709 row: i column: 09
High quality sequence stop: 757.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/clone lib="MIH MGC 109"
/clone lib="WIH MGC 109"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoR1; Site_2:
Xho1; cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/Xho1 sites using the following 5' adaptor:
GGGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library.
331 c 260 g 190 t
                                                           cloned
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 657)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
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                                                                                                                                                                                                                                           Score 394.2; DB 13; Length 944; Pred. No. 1e-63; 0; Mismatches 88; Indels 1;
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CB444165.1 GI:29233914
                                                                                                                                                                                                                                         tch 71.0%; al Similarity 83.7%; 458; Conservative
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( bases 1 to 944)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           772 AGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTTGCATTGAGAACAGCTTCATGACT
     CACAGCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCA
                                        GGGCTGGCCGGCACCTTCCGGGCCTTCCTGTCGCGGCTGCAGGACCTCTACAGCATC
                                                                                                                                                   GGGCTGGCGGCCACCTTCCGCGCCTTCCTCCTCGCGCCTGCAGGACCTGTACAGCATC
                                                                                                                                                                                                                                                              CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCAGCTGAAGCCCGGGGCCCGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2899 row: d column: 04
High quality sequence stop: 572.
                                                                                                                                                                                       GTGCGCCGCGCCGACCGCACCGGGGTGCCCGTCGTCAACCTCAGGGACGAGGTGCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGENCOURT_10434549 NIH_MGC_109 homo sapiens cDNA clone IMAGE:6650260 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGCCCCCGGCGGCCACCGGCCACGTCGTCGCTGCTGCTGGCGGCGGCAGGC
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/organism="Homo sapiens"
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Homo sapiens (human)
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Best Local Similarity
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BUG15520
BUG15520.1 GI:23281735
EST.
                                                                                                                                      Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: FQX8051 column: 11
Seq primer: TAGAAGGCAAGTCGAGG.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCCCCGACTITCAGTGCTTCCAGCAGCGCGCGCGCGGGGGCTGGCCGGCACATTCC 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 GGCAGGCGTCGCTGCTGCTGCCGGGCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCC 499
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                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9913"
/tismue_type="pooled"
/tismue_type="pooled"
/clone_lib="MARC_6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537 CCACCCTGCCCGTCGTCAACCTCAGGGACGAGGTGCTGTTTCCTAGCTGGGAGGCCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 t
                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                        /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 423; Conservative
                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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DEFINITION

ACCESSION VERSION KEYWORDS

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/done libs-"NCI CGAP END .
//done libs-"NCI CGAP END 2:
//done coll line (2 cell lines). The libs-ray was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into py773-Pac vector. The oligonocleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGGTCACTC. The cell lines was provided by Dr James Martin from University of lowa.
                                                                                                                                                                                                                                                                                                                                                           CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa from Dr. M. Bento Soares, Destribution information can be obtained from Dr. M. Bento Soares, bento-soares@ulowa.edu

The following repetitive elements were found in this cDNA sequence: 1-44, >POLY A#Simple_repeat (matched compliment)

Seg primer: M13 FORWARD
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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TAG TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
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Pred. No. 6.5e-62;
0; Mismatches 77; Indels
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/tissue_type="Enchondroma cell line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .703
/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref="taxon:9606"
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RESULT 8 BQ672290 LOCUS DEFINITION

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

BASE COUNT ORIGIN

Matches

340

음 ò a ò g ò g ò 셤

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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Lowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
227 CACAGCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                         TICTCTTTCGACGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGAAGAGCGTGTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGCCCCGGCGCCCACCGGCCAGGCCTCGTCGCTGGCGGCCAGG---CTGCTGGAG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 683)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                         287 GGGGGCATGCGGGGCTTCCGGCTTCCAGTGCTTCCAGCGCGGGCCGTG
                                                                                                                                                                                                                                                                                                                                         CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  707 AGAĞTGCCCGCGAGCTGCCATCACGCCTACATGTGCTCTGCATTGAGAACCGCTTCATG
                                                                                                                                                                   407 GTGCGCCGTGCCGACCGCGCGGCCGTGCCCATCGTCAACCTCAAGGACGACGTGCTGTTT
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                                                                                                                                             GGGCTGCCGGCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATC
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UI-E-EO1-ajd-g-02-0-UI.sl UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-ajd-g-02-0-UI 3', mRNA sequence.
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The following repetitive elements were found in this cDNA
sequence: 1-44, >POLY_A#Simple_repeat (matched compliment)
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97044477
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/lab_host="DH10B (phage-resistant)"
/clone_lb="NH1MGC_102"
/clone_lb="NH1MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1XAno sites using the
following 5' adaptor: GGGACAGG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGENCORT 8354946 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275261

S, mRNA sequence.
                           400
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                                                                                                                                                                                                              339 TACTGTGAGACGTGGCGGACGCAGGCTCCCTCGGCCACGGCCAGGCCTCCTCGCTGCTGCTG 280
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                                                                                                                                                                                                                                                                                                                     279 GGGGGCAGGCTCTTGGGGCAGAGTGCCGCGAGATGCCATCACGCCTACATCGTGCTCTGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMA458 row: c column: 06
High quality sequence stop: 588.
Location/Qualifiers
I. 929
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399 TGGCCCCAGAAGAGGCGTGTGGCATGGCTCGGACCCCCAACGGGCGCAGGCTGACCGAGAGC
                                                                                                                                                                           TACTGCGAGACGTGGCGGACGGAGGCCCCGGCGGCCACCCGGGCAGGCGTCGTCGCTG
                                                                                                                                                                                                                                                                        460 GCGGGCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGC
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Pred. No. 7.2e-62;
0; Mismatches 93; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                     520 ATCGAGACAGCGTCATGACCTCCTTC 546
                                                                                                                                                                                                                                                                                                                                                                                                 219 ATTGAGAACAGCTTCATGACTGCCTCC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6275261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ672290.1 GI:21783124
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82.5%;
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Best Local Similarity
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AWUUUSB3 682 bp mRNA linear EST 15-OCT-1999 8202603.x1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2594333 3' similar to SW:CAIH HUMAN P39060 COLLAGEN ALPHA 1(XVIII) CHAIN [CONTAINS: ENDOSTATIN]: mRNA commonder
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 682)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: polyr not found Seq primer: -400P from Gibco High quality sequence stop: 408.

Location/Qualifiers
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Pred. No. 1.8e-60;
0; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnI.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                         AW089583.1 GI:6046927
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                                                                                                                                                                                                                                     Homo sapiens (human)
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Matches 424; Conservative
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Unpublished
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                                      RESULT 10
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                                                                                                                                     /docome="UT-E-EO1-agid-g-02-0-UI"
/tissue_type="fetal eye"
/docome="UT-E-EO1-agid-g-02-0-UI"
/tissue_type="fetal eye"
/dev_fadge="fetal"
/lab_host="DH010B [Life Technologies] (T1 phage resistant)"
/lab_host="DH010B [Life Technologies] (T1 phage resistant)"
/clone_lib="U1-E-EO1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye: The library was constructed according to Bonaldo, lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT7)18 tail. The sequence tag for this library is CGGGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 GCAGAGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATTGAGAACAGCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGGGGCTGGCCGGCCACCTTCCGGGCCTTCCTGTCGTCGCGGCTGCAGGACCTCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622 CGTGGGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCCTGCAGGACCTGTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 CTTCCCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGCCCAGCTGAAGCCCGGGGCCCG
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Pred. No. 1.5e-60;
0; Mismatches 71;
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TAG_TISSUE=human fetal eye
TAG_SEQ=CGCGTATACC"
132 t
                                                                                   organism="Homo sapiens
                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                        Location/Qualifiers
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primer: M13 Forward
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Best Local Similarity 85.5%;
Matches 419; Conservative
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I (Dases 1 to 874)
I (Dases 1 to 874)
I (Dases 1 to 874)
IS NIH-MGC http://mgc.nci.nih.gov/.
IN Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgappa-remenl.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAW1361 row: g column: 18
High quality sequence start: 23
High quality sequence start: 23
High quality sequence start: 23
Llocation/Qualifiers
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602990468F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5146409 5',
mRNA sequence.
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   231 GGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGCTTCCAGCAAGCCCGAGCCGTG 290
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                                                                                                 481 GAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTGCATCGAGAACAGCGTCATGACC
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/lab_host="DH10B (phage-resistant)"
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/clone="IMAGE:5146409"
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/strain="CZECH II"
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                                                                                                                                                                 382 TGGCCCCAGAAGAGCGTGTGGCATGGCTCGGACCCCAACGGGCGCAGGCTGACCGAGAGC 323
                                                                                                                                                                                                                                TACTGCGAGACGTGGCGGACGGAGGCCCCCGGCGGCCACCGGGCAGGCGTCGTCGCTGCTG 459
                                                                                                                                                                                                                                                                                   322 TACTGTGGGGGGGGGGGGGGCTCCCTCGGCCACGGGCCTCCTCCTCGCTGCTG 263
                                                                                                                                                                                                                                                                                                                                                             460 GCGGGCAGGCTGCTGGAGCAGGAGGCCGCGAGCTGCCGCCACGCCTTCGTGGTGCTCTCTGC 519
                                                                                                                                                                                                                                                                                                                                                                                              262 GGGGCCAGGCTCCTGGGGCCGAGGTGCCGCGAGCTGCCTCATCACGCCTACATCGTGCTCTGC 203
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:4195660"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/clone lib="MYCI CGAP Li9"
/note="Organ: līver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapDs-remail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMPSJI row: i column: 05
High quality sequence stop: 761.
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Pred. No. 2.6e-60;
0; Mismatches 112; Indels
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/mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30299651"
/lab_host="DH10B (T1-phage-resistant)"
/clone lib="NHH MGC 118"
/note="Organ: lung and heart; Vector: pDNR-LIB; Site_1:
                                                                                                                                            CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 12 http://image.llnl.gov column: 12 High quality sequence stop: 567.

Location/Qualifiers
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0; Mismatches 112; Indels
                               Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 715)
NIH-MGC http://mgc.nci.nih.gov/.
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AGENCOURT_8414390 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6272287
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 979)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2450 row: g column: 08
High quality sequence stop: 638.
Location/Qualifiers
I. 979
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CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC
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                                                                                     TTCTCTTTTCGACGCAGAGATGTCCTGCAGCACCCCGCCTGGCCCCGGGAAGAGAGGTGTGG
                                                                                                            CACGGCTCCGACCCCAGCGGCGCC--GCCTGACCGACAGCTACTGCGAGACGTGGCGGA
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                                        cccagcrossascercrosrcrossecrorsascerccecrosasceccesses
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.9e-59;
0; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5', mRNA Sequence.
BQ673186
BQ673186.1 GI:21784020
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Best Local Similarity 83.1%;
Matches 458; Conservative
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clong_lib="NIH MGC]85"
/notes="Organ: Colon; Vector: pOTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGGG(G). Size-selected by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
99 a 320 c 265 g 118 t
                                                                                                                                                                      BG387051 832 bp mRNA linear EST 12-MAR-2001 602454749F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4582933 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contect: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1306 row: a column: 14
High quality sequence stop: 679.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 832)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:4582933"
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                      CCTTCTCCAAGIAG 555
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E34473 Carrier/DNA
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                  GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Homo sapi Homo sapi

AX399631 Sequence AX399629 Sequence

Description

AF189709 Rattus no AX370853 Sequence AJ236873 Rattus no

AF083440 Gallus ga AB047066 Xenopus l AY052763 Xenopus l

RESULT 2  AX399629 LOCUS  DECUSS  DEFINITION Sequence 1 from Patent EP1191036.  ACCESSION AX399629.1 GI:21335409  KEYMORDS  SOURCE Canis familiaris CRGANISM Canis familiaris CRGANISM CANISM CANISM EMPTRENCE THE MARMMALIA; Butheria; Carnivora; Fissipedia; Canidae; Canis.  AUTHORS AUTHORS AUTHORS TITLE INVOLVING and TONG,X. FEATURES 1. Cocation/Qualifiers 1. Cocation/Qualifiers 1. Cocation/Qualifiers 1. AD2 AD2 AND	Ment Scores: 1.69e-69 Length: No.: 966.00 Matches: nt Similarity: 100.00\$ Mismarch Match: 66.00\$ Indels:	US-09-938-391-4 (1-184) x AX399629 (1-829)  Qy		101 PheSerPheAspGlyArgAspValLeuGlnHisProArgLyCascaceConnergy 101 PheSerPheAspGlyArgAspValLeuGlnHisProArgTyproArgLySerValTrp 12 132 TTCTTTCGGGGGGAGGAGGTCTGCGGCCCGGGGAGGCGTGGG 49 121 HisGlySerAspProSerGlyArgArgTcTGGAGCCTGGCCCGGGAGGCGTGGG 49 121 HisGlySerAspProSerGlyArgArgTagLeuThrAspSerTyrCysGluThrTrpArgThr 14 141 GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 16 141 GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 16 159 GAGGCCCGGCGCGCGCGCCTCGCTCGCTGGCGAGCGGGGGGGG
LOCUS LOCUS DEFINITION Sequence 3 from Patent EP1191036. DEFINITION Sequence 3 from Patent EP1191036. DEFINITION AX399631 AX39963	ignment Scores:  1.09e-69 Length: 555  ed. No.: 966.00 Matches: 184  ore: 966.00 Matches: 184  crent Similarity: 100.00\$ Conservative: 0  st Local Similarity: 100.00\$ Indels: 0  ery Match: 6 2 Gaps: 0  -09-938-391-4 (1-184) x AX399631 (1-555)	0y 1 HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro 20 1	121   GGCTGGCCGCCCTTCCGGGCCTTCTTCGTCGTCGTCGTCG	

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PAT 02-APR-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Boerner, R.J., Bermejo, L.L., Mistry, F.R., Shepard, S.R. and
Schrimsher, J.L.
Method of producting and purifying endostatin? tm protein
Latent: WO 0119989-A 4 22-MAR-2001;
EntreMed, Inc. (US)
Location/Qualifiers
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// Coganism="Homo sapiens"
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                                                                                                                                                                                                                                                                             Unclassified.

1 (bases 1 to 546)

1 (bases 1 to 546)

1 (bases 1 to 546)

2 (bellly, M.S. and Folkman, M.Judah.

Therapeutic antiangiogenic endostatin compositions

Therapeutic antiangiogenic endostatin

Therapeutic antiangiogenic endostations

Therapeutic antiangiogenic endostations

Therapeutic endos
                                                                                                                     linear
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Conservative:
Mismatches:
Indels:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Angiogenesis-inhibiting peptides and proteins and met
Parent: WO 0230982-A 2 18-APR-2002;
EntreMed, Inc. (US)
Location/Qualifiers
1. 552
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NT 83 a 196 c 179 g 94 t
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Sequence 2 from Patent WO0230982.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 30 from Patent WO0193897.
AX395662
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FIRSPGRDVLRHPTWPQKSVWHGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGR
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/note="similar to endostatin; can inhibit endothelial cell
proliferation"
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Feng,Y., Cui,L.B. and Ma,Q.J.
Direct Submission
Submitted (0.3 SEP-2001) Genetic Engineering, Beijing Institute of Biotechnology, Taiping Road, Beijing 100850, P.R. China
Location/Qualifiers
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                                                                                                                                              HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
                                                                       GlualaalaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr
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Fengy Y., Wu, Y., Zhu, X., Liu, C.X. and Ma, Q.J.
Endostatin contributes to maintain cartilage homeostasis via
promotion of the anabolic program of chondrocytes
Unpublished
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Homo sapiens collagen XVIII mRNA, partial cds.
AF416592
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Sheng Wu Gong Cheng Xue Bao 17 (3), 278-282 (2001)
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1 (bases 1 to 52)

Bolanowski,M.A., Caparon,M.H., Casperson,G.F., Gregory,S.A., Klein,B.K. and Mckearn,J.P.
Fused protein containing angiostatin component and utilization thereof in anticunor therapy
Datent: JP 2001518304-A 50 16-OCT-2001;
Datent: JP 2001518304-A 50 16-OCT-2001;
Pused Bono sapiens (human)
Pub 16-OCT-2001
                                                                                                             552 bp DNA linear PAT 27-AUG-2002 Fused protein containing angiostatin component and utilization thereof in antitumor thereof
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Fused protein containing angiostatin component and utilization
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BARBARA K KLEIN, JOHN P MCKEARN
C12N15/097A61K38/00,A61K48/00,A61P9/10,A61P35/00,C07K14/52,
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01-OCT-1997 US 60/060609
MARK A BOLANOWSKI, MAIRE H CAPARON, GERALD F CASPERSON, SUSAN
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Sequence 12 from Patent W00210372.
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Homo sapiens multi-functional protein MFP mRNA, complete cds.
AF282883
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Submitted (27-JUN-2000) R & D, Robinson Biotech Corp., 24634 Five Mile Road, Suite 24-26, Redford, MI 48239, USA Location/Qualifiers
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Razusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomicséhri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                Oshima, A., Takahashi-Pujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y. Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
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Unpublished
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                              Chapman, P.W., ge Luca, G. and Falciola, L. Method of producing functional protein domains teams: WO 021037-A 12 07-FEB-2002; Applied Research Systems ARS Holding S.A. (AN)
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Contact: MGC help desa
Contact: MGC help desa
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter.N., Ayels.K., Beckstrome.Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Boufffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Blakesley,R.W., Ganite,S.L., Kavins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Malker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC033715 2637 bp mRNA linear PRI 08-JUL-2002 Homo sapiens, Similar to collagen, type XVIII, alpha 1, clone IMAGE:4425380, mRNA, partial cds.
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Catarrhini; Hominidae; Homo.
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Direct Submission

Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Submitted (02-JUL-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                               1944 TTCTCCTTTGACGGCAAGGACGTCCTGAGGACCCCACCTGGCCCCAGAAGAGGGGTGTGG
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                                    PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp
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/db_xref="taxon:9606"
/clone="IMAGE:4425380"
/tissue_type="Kidney, hypernephroma"
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates;
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1 (bases 1 to 3394)
Olsen, B.R. and Oh, S.P.
Collagen and uses therefor
Patent: US 5643783-A 4 01-JUL-1997;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                             1. 3394
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="teaxon:9606"
/note="EMBL/GenBank Accession No. L22548"
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/product===collagen type XVIII alpha 1"
/product==collagen type XVIII alpha 1"
/product==collagen type XVIII alpha 1"
/db_xref="collagen" to a collagen type XVIII alpha 1"
/db_xref="collagen" type XVIII alpha 1"
/db
                                                               Human collagen type XVIII alpha 1 (COL18A1) mRNA, partial cds. L22548 L122548.1 GI:348908. Alpha 1 L22548.1 GI:348908.
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GGFFGSSLPGARDARDGPRGYPGTPGRESIRGOQPBPGRQGAPPGGTGSTGRQQPBCDP
GGFFGSSLPGARDARGPRGYPGTPGPPGPPGPGTMGASSGQVRLWATRQAMLGQVHEVP
GGPRESPFPGPRQTI SVPCPPGPPGPPGPPGTMGASSGGVRLWATRQAMLGQVHEVP
EGWLIFVAEQEELYRVUQNGFRKVQLEARTPLPRGTDNEVAALQPPVVQLHDSNPYPR
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PVLHLVALNSPLSGGWRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRAD
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DPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSFWTA
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                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (b. 23394)

Oh.S.P., Marman, M.L., Seldin, M.F., Cheng, S.D., Knoll, J.H., Timmons, S. and Olsen, B.R.

Timmons, G. cDNA and genomic DNA encoding human type XVIII collagen and localization of the alpha 1(XVIII) collagen gene to mouse chromosome 10 and human chromosome 21

Genomics 19 (3), 494-499 (1994)
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Location/Qualifiers
1. .3394
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/db_xref="taxon:9606"
/map="21q22.3"
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/dev_stage="adult"
1. 3394
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Homo sapiens (human)
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1624 GGGCTGGCGGGCCTTCCGGGCCTTCCTGCGGCCCTGCAGGACCTGTACAGCATC 1683
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41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                           61 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
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DNA encoding human
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-MODEL=frame+ pln.model -DEV=xlp
-MODEL=frame+ pln.model -DEV=xlp
-MODEL=frame+ pln.model -DEV=xlp
-Cgn2_1/USPTO_spool_p/US09938391/runat_04082003_130655_27077/app_query.fasta_1.718
-DB=N Geneseq_19Jun03_-OFWT=fastap_-SUFFIX=pln.rng_-MINMATCH=0.1_-LOOPCL=0
-LIST=E -DOCALIGN=200 -THR SCORE=pct_THR MAX=100 -THR MIND=0.ALIGN=15
-MODEL=LOCAL_-OUTPWT=pco_-NORM=ext_-HEAPSIZE=500_-MINLEN=0_-MAXLEN=200000000
-USRE=US09938391_@CGN 1_1_605_@runat_04082003_130655_27077_-NCPU=6_-ICPU=3
-NO_MMAP_-LARGEQUERY_-NGG_CGORES=0_-MAXIT_DSPELOCK=100_-LONGLOG
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version 5.1.6
- 2003 Compugen Ltd.
                                                                                             OM protein - nucleic search, using frame_plus_p2n model
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ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; gynaecological; gene; ss.
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Matches:
Conservative:
Mismatches:
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/note= "no start codon"
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                                                                                                                           Location/Qualifiers
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P-PSDB; AAO17430.
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                              241 CCCAGCTGGGAGGCCTTATTCTCGGGCTCCGAGGGCCAGCTGAAGCCCGGGGCCCGCATC
ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArgIle
                                                                                                                                                                     301 TTCTCTTTCGACGGCAGAGATGTCCTGCAGCACCCGGCCTGGCCCCGGAAGAGCGTGTGG
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/product= "pro-endostatin"
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P-PSDB; AAO17429.
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06-JUN-2000 (first entry)

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pro-endostatin and endostatin. The sequences can be used in the treatment and diagnosis of angiogenesis related disorders, including cancer, theumatoid arthritis, psoriasis, retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiactasia, haemophiliac joints, angiofibroma, wound granulation, coronary collaterals, cerebral collaterals, arteriovenous malformations, isohaemic limb angiogenesis, diabetic neovascularisation, and fractures. The present sequence is the canine pro-endostatin coding sequence.
                                                                                                                                                                                                                                                          Sequence 829 BP; 124 A; 314 C; 278 G; 113 T; 0 other;
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                 Claim 2; Fig 2; 56pp; English.
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                                                        GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
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Percent Similarity: Best Local Similarity:

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AAZ51309 standard; DNA; 552

RESULT 3
AAZ51309
ID AAZ5
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AC AAZ5
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AAZ51309

619

Query Match: DB:

Alignment Scores:

Length: Matches:

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a signal sequence, an immunoglobulin Fc region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours that may be treated include solid tumours, blood born tumours tumour metastasis, benigh tumours including haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses a DNA molecule encoding a fusion protein comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plague neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation endothelial cells, intestinal cells, atherosclerosis, sclerodermal and hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encoding canine endostatin used in the construction of immunofusin containing canine
                                                                                             angiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy; ds.
                                                                                Canine; immunoglobulin Fc fragment; endostatin; immunofusin;
                                                                                                                                                                                                                                                                                                                                                                                  /note= "Does not include stop codon"/partial
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                                     Canine angiogenesis inhibitor, endostatin DNA.
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P-PSDB; AAY70265.
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98US-0106343. 99US-0315689.

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121 HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr 140
                                                                                                              Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers
                                                                                                                                                         Claim 10; Page 39; 68pp; English
                                         (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                      and as birth control agents
                                                             Folkman MJ;
                                                                                  2000-365617/31.
                                                                                            P-PSDB; AAY94323
        30-OCT-1998;
20-MAY-1999;
                                                             O'Reilly MS,
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                                           GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
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                                                                                                                 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                          ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; endothelial cell proliferation inhibitor; collagen XVIII; angiogenesis inhibitor; anti-tumour; cytostatic; antipsoriatic; vasotropic; determatological; ophthalmological; vulnerary; antiarteriosclerotic; antidabetic; haemostatic; contraceptive; coular angiogenic disease; atherosclerosis; scleroderma; myocardial angiogenesis; telangiectasia; angiofibroma;
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/*tag= a
/product= "Endostatin protein"
        US-09-938-391-4 (1-184) x AAZ51309 (1-552)
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The present sequence encodes an endostatin protein which is the carboxy terminal protein of human collagen XVIII. Recombinant mouse endostatin (20 mg/kg) was administered subcutaneously to mice implanted with Lewis lung carcinomas. There was tumour mass regression non-detectable levels after 12 days of therapy due to the angiogenesis inhibitory activity of endostatin. Thus the protein is useful for treatment of angiogenesis, capacity of endostatin are useful for treating and diagnosis of tumours, ocular endostatin are useful for treating and diagnosis of tumours, cular plaque neovascularisation, telanglectasia, haemophiliac joints, angiogenic diseases, Osler-Webber syndrome, myocardial angiogenesis, plaque neovascularisation, telanglectasia, haemophiliac joints, angiotibroma and wound granulation, for treatment of diseases related to excessive or abnormal stimulation of endothelial cells e.g. intestinal adhesions, atherosclerosis, scleroderma. The protein may also be useful cas a birth control agent by reducing or preventing uterine
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US-09-938-391-4 (1-184) x AAX77719 (1-549)
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                                                                                    161 GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine endostatin and angiostetin, human or murine endostatin and angiogenesis-inhibiting fusions and fragments, where the viral vector-is sufficiently attenuated for use in human gene therapy. The products of phthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retinn. The vector is administered to cells ex vivo and then administered to the patient.
                                                                                                                                                                                                                                                                                                             Plasminogen, human, angiostatin, endostatin, gene therapy, vector; anti-angiogenic; attenuation, cytostatic, anti-diabetic, ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina; ss.
GAGGCTCCCTCGGCCACGGCCAGGCCTCCTCGCTGGGGGCAGGCTCCTGGGGCAG
                                                                                                    AGTGCCGCGAGCTGCCATCACGCCTACATCGTGCTCTGCATTGAGAACAGCTTCATGACT
                                    GlualaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                      Human endostatin DNA coding region fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENETIX PHARM INC.
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pawliuk RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-angiogenic gene therapy vectors
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                                                                                                                                                                                                              AAX77719 standard; DNA; 549 BP
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P-PSDB; AAY08693.
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GCC 543
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Mismatches:
Indels:

2.67e-73 835.00 92.82% 85.08% 86.44%

Score:
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Pest Local Similarity:
Query Match:
DB:

Gaps:

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                                                          GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla 40
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HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro 20
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                181 Grececciecceacceaccerecerecereicareicaacereaceaccaecrecierr
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                                                                                                                                                                                   ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
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P-PSDB; AAY90771.
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GCC 543
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Human angiogenesis inhibitor, endostatin cDNA.

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                                                                  The present sequence encodes an angiogenesis inhibiting factor (1), designated IAF-1. The present invention also describes: (1) preparation of (1) and its derivative; (2) an IAF binding acceptor and its preparation; and (3) an IAF antibody. (1) is useful for preparing new biological preparations for effectively treating various tumours and abnormal-vessel diseases. The IAF antibody is preferably a polyclonal antibody, mosaic antibody, single stranded antibody and human originated
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Angiogenesis inhibiting factor 1 and its derivative useful for treating
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Matches:
Conservative:
Mismatches:
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                                        Example 1; Fig 5; 41pp; Chinese
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835.00
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The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis chibibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metestasis, benign tumours including. The meangiomas, acoustic neuronas, neurofibromas, trachomas and pyrogenic granulomas, theumatoid arthritis, psoriasis, ocular angiogenic diseases c. g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental collibroma, wound granulation, telangiectasis, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a CDNA encoding human constructs in gene therapy. The present sequence is a cDNA encoding human
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refers to this sequence as being nucleotide sequence of human endostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel fusion protein of angiostatin or endostatin and an immunoglobulin
                                                 Human; immunoglobulin gamma Fc fragment; endostatin; immunofusin; angiogenesis; inhibitor; cytostatic; antirheumacoid; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; coular angiogenesis; plaque neovascularisation; diabetic retinopathy; macular degeneration; wound granulation; keloid scar; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin gamma (IgG) Fc fragment.
Note: This sequence is stated in claim 12 as being amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -
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*tag= a /product= "Endostatin"
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/note= "Does not include stop codon"
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Conservative:
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                                                                                                                                                                                                                                                                         Location/Qualifiers
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reaction of Pichia pastoris harbouring an expression
plasmid containing the present sequence"
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y FR, Shepard SR,
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                                               HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro
                                                                                         GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
                                                                                                                                                                                   CCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCACGCATC
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                                                                                                                                                                                                                                                                                              HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
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                                                            GCCGCCATGCCGCGCGCCCGCCCGACTTCCAGTCCTTCCAGCAGCCGCGCGCCGTG
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                            US-09-938-391-4 (1-184) x AAZ51291 (1-549)
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The sequence encodes Human Endostatin(TW). The new method of the invention is useful for producing, recovering and purifying Endostatin convention is useful for producing, recovering and purifying Endostatin culture media, and fermentation media. Endostatin(TW) is useful for treating angiogenesis mediated diseases such as solid tumours, blood control tumours, leukaemias, tumour metastases, benign tumours, blood control tumours, leukaemias, tumour metastases, benign tumours, e.g. control tumours, retumours neurofibromas, trachomas, and pyogenic granulomas, rheumatcoid arthritis, psoriasis, ocular angiogenic diseases, control trachomas, rheumatcoid arthritis, psoriasis, ocular angiogenic diseases, control granulomas, retrolental fabroplasia, rubeosis, osler-Webber Syndrome, cancer, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, colon cancer, retrolental fibroplasia, rubeosis, osler-Webber Syndrome, contemporation disease of excessive or abnormal stimulation of endothelial cells such as intestinal adhesions, atherosclerosis, colon contential cells such as intestinal adhesions, atherosclerosis, color colorisatin(TW) can be stored in buffers for extended periods of time, and cologically active Endostatin(TW) are obtained by the new method.

Endostatin(TM) can be stored in buffers for extended periods of time, or also subjected to lyophilsation, while preserving biological activity.

C centrifugation of broth from fermentation steps in production is avoided, of abrief and proteins, pigments, enzymes and other cellular chemicals and adherenced and and adherenced and adherenced and activity and other cellular special such and adherenced and activity and additional proteins, pigments, enzymes and other cellular cellular specials and other cellular specials and selected and acti
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                                                                                                                                                                                                                                                   reaction of Pichia pastoris harbouring an expression plasmid containing the present sequence"
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product= "Endostatin(TM) C-terminus minus 2"
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l, Schrimsher JL;
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kringle domain; cell proliferation; viral vector;
replication-defective; cancer; tumour; ss.
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the specification as an amino acid sequence.
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HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces sp. strain C5; SnpA; S. venezuelae; alpha-amylase;
endostatin; cancer; tumour growth; angiogenesis; ss.
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/product= "endostatin"
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/*tag= a
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                    AGTGCCGGAGCTGCCATCACGCCTACATCGTGCTCTGCATTGAGAACAGCTTCATGACT
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                                                                                                                                                                                                                                                                                      Angiostatin; endostatin; interferon; thrombospondin; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis;
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                                                                                                                                                                                                                                                                                                                                                         tumor cell production; ss.
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Klein BK, McKearn JP;
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in Streptomyces. Leader sequences of Streptomyces sp. strain CS. SnpA and S. venezuelag alpha-amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer, inhibition of tumour growth, inhibition of angiogenesis, isolation of receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation for cultivation in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced.
                                                                                                                                                                                                                                 present sequence encodes human endostatin. The protein is expressed
                                                Preparation of soluble recombinant endostatin involves transforming Streptomycete host with expression vector comprising nucleotide sequence encoding endostatin operably linked to linker and leader
                                                                                                                                                                                 Example 1; Fig 6; 57pp; English.
P-PSDB; AAB30493
                                                                                                                                peptide
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Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;

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res: 2.69e-73 835.00 82.82\$ milarity: 85.08\$ 21.44\$	91-4 (1-184) x AAC62023 (1-552)	1 HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro	1 CACAGCCACCGCGACTTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCTGTCA	21 GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla	61 GGCGGCATGCGGGGCATCCGCGGGGCCGACTTCCAGTGCTTCCAGCGCGCGC	41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle		61 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe	1 GTGCGCCGTGCCGTGCCGTGCCCATCGTCAACCTCAAGGACGACGGCTGTTTTTTTT	81 ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArgIle	CCCAGCTGGGAGGTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGGCACGCATC	PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpPro	1 TTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCCACCTGGCCCCCAGAAGAGCGTGTGG	1 HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr	CATGGCTCGGACCCCAACGGGCGCAGGCTGACC	GlualaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln	GAGGCTCCCTCGGCCACGGCCTCCTCGCTGGGGGGCAGGCTCCTCGGGGGCAG	GluAlaAlaSerCysArgHisAla	1 AGTGCCGCGAGCTGCCATCACGCCTACGTGCTCTGCATTGAGAACAGCTTCATGACT
nent Sc No.: It Simi Local S Match:	٠,			7	9	4	121	9	181	80	241	101	301	121	361	141	421	161	481
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Length: Matches: Conservative: Mismatches:

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Best Local Similarity:

Percent Similarity:

Alignment Scores:

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Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;

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This invention relates to angiogenesis-inhibiting protein receptors, and the DNA sequences encoding them. Angiogenesis is the generation of new blood vessels into a tissue, and normally occurs in wound healing, feetal and embryonal development and the formation of the corpus luteum, feetal and embryonal development and the formation of the corpus luteum, and placenta. Angiostatin is a protein (see AAB16450 and AAA68202) involved in angiogenesis, and has an amino acid sequence similar to that of a plasminogen fragment (see murine plasminogen to that of a plasminogen fragment (see murine plasminogen angiogenesis). Sequences AAA68242 and AAB16522 represent coding and protein sequences of human laminin. Laminin is an angiostatin binding protein. Sequences AAB16452 and AAB16522 represent coding and protein. Sequences of human laminin is an angiostatin binding protein. The cand some of the peptides of the invention share homology with regions of laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the angiosenesis-inhibiting protein receptor fragments of the invention. The peptides bind either angiostatin or endostatin and can be used in methods corpus as solid tumours, psoriasis, scleroderma, myocardial angiogenesis, crohn's diseases and processes that are mediated by angiogenesis. Crohn's disease, cerebral collaterals, arteriovenous malformations, theories, diabetic retinopathy, arthritis, wound healing, peptic ulcers, Helicobacter related diseases, fractures, placentation and cat scratch fever. They are useful for the detection and prognosis of cancer. DNA sequences A628204-A628211 encode the peptides of the invention.
                                                                                                                                                                                                                                                                                          Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin; endostatin; plasminogen; laminin; treatment; wound healing; solid tumour; psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease; cerebral collateral; arteriovenous malformation; rubeosis; cancer; diabetic retinopathy; arthritis; wound healing; peptic ulcer; Helicobacter related disease; fracture; cat scratch fever; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New angiogenesis-inhibiting protein receptors, useful in methods for treating diseases and processes that are mediated by angiogenesis, such as solid tumours, psoriasis, scleroderma and myocardial angiogenesis -
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AAC88289 standard; DNA; 552 BP.
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                                                                                                                                         The present sequence encodes human endostatin, an angiogenesis inhibitor, derived from human liver cDNA. This is the C-terminal protecolytic fragment of collagen 18a. Endostatinn can inhibit endothelial cell proliferation in vitro and angiogenesis in vivo. This is used in the construction of the expression plasmid for the treatment of mammalian diseases, especially cancer. The plasmids can be used for (in vivo) transfection of a cell in situ in order to modulate tumour activity. Anti-angiogenic gene inhibits growth of solid tumour and lung metastatic tumours by intravenous or intramuscular delivery.
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Plasmids comprising tissue specific transcription elements linked to anti-angiogenic gene is useful transfection of cells and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 AGCGCCGCCAGCTGCCACCACGCCTACATCGTGCTGTGCATCGAGAACAGCTTCATGACC
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                                                                                                Disclosure; Page 40; 103pp; English
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92.82%
85.08%
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120 360 140 420

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480

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GlualaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 160
GTGCGCCGTGCCGACCGCGCAGCCGTGCCCATCGTCAACCTCAAGGACGAGCTGCTGTTT 240
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                                                                                                                                                                                                                                                                                                                                                             481 AGTGCCGCAGAGCTGCCATACATCGTGCTTTGATGAGAACAGCTTCATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regulating angiogenesis for treating scleroderma, leukaemia, keloids badministering a protein that is homologous to PITSLRE protein kinase and an angiogenic factor or a protein kinase and its active fragments
                                       ProserTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArgIle
                                                                          CCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCCGGGGCACGCATC
                                                                                                                                  PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp
                                                                                                                                                                                       HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
                                                                                                                                                                                                                        361 careecreegaceceaaceegeegeagecreacegagageracrergagaceregegeace
                                                                                                                                                                                                                                                                                                                                       161 GlualaalaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product= "Endostatin"
/note= "This sequence lacks a start codon"
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancers, inflammation, rheumation arthritis, chronic articular rheumatism, psoriasis, disorders associated with inopportune invasion of prematurity, acular degeneration, corneal graft rejection, retrolental fibroplasia, rubeosis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent neconsequication, reheave syndrame, mycoardial angiogenesis, plaque neconsequisation, telangiectasia, hemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGCGGCATGCGGGGCATCCGCGGGGCCGACTTCCAGTGCTTCCAGCAGGCGCGGGGCCGTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endostatin peptide comprising at least four endostatin amino acid residues are e.g. angiogenesis inhibitors for treating cancer and diabetic retinopathy.
                                                                                                                              Endostatin; antiangiogenic; angiogenesis; human; mouse; cancer; inflammation; angiogenesis-dependent disease; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                           Human endostatin coding sequence SEQ ID NO: 1
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835.00
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                                                      (first entry)
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                   AAC88289;
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Search completed: August 17, 2003, 20:06:34 Job time : 220.778 secs

angiogenesis. The method comprises administering to a human or animal a composition comprising a protein that is homologous to PITSLRE protein kinase (PK) and an angiogenic factor. The method is useful for regulating angiogenesis related to cancer, arthritis, macular degeneration, and diabetic retinopathy. The compositions are useful for inhibiting angiogenic retinopathy. The compositions are useful compositions are useful in treating diseases. The method and compositions are useful in treating diseases and processes that are mediated by angiogenesis including haemangioma, solid tumours, blood borne tumours, leukaemia, metastasis, telangiectasia, psoriasis, collacterals, arteriovenous malformations, ischaemic limb angiogenesis, collaterals, arteriovenous malformations, ischaemic limb angiogenesis, corneal diseases, rubeosis, neovascular glaucoma, diabetic retinopathy, macular degeneration, wound healing, peptic ulcer, Helicobacter related diseases, fractures, keloids, vasculogenesis, haematopoiesis, ovulation, macular degeneration, and cat scratch fever. The method of the invention provides a therapy for cancer that has minimal side effects. The present sequence encodes human endostatin which is used to generate angiogenesis-inhibiting peptides. The present invention relates to methods and compositions of inhibiting 

Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;

Alignment Scores:			
Pred. No.:	2.69e-73	Length:	552
Score:	835.00	Matches:	154
Percent Similarity:	92.82%	Conservative:	14
Best Local Similarity:	85.08%	Mismatches:	13
Query Match:	86.44%	Indels:	0
DB:	24	Gaps:	0

US-09-938-391-4 (1-184) x ABK50685 (1-552)

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1 HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro	GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle	ValargargalaaspargThrGlyValProValValasnLeuArgaspGluValLeuPhe	ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArgIle	. PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 	. HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCygGluThrTrpArgThr 	GIUALAPTOALAAIATHKGI YGINALASerSerLeuLeuAlaGI yArgLeuLeuGluGIn	. GlualaalaSerCysargHisAlaPheValValLeuCysIleGluAsnSerValMetThr 
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Patent No. 6346510

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FOLKman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
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TYPE: DNA ORGANISM: Homo sapiens
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/CG012_1/USFPTO spool_p/US938391/runat_04082003_130656_27125/app_guery.fasta_1.718
-Q=/CG012_1/USFPTO spool_p/US9938391/runat_04082003_130656_27125/app_guery.fasta_1.718
-DB=ISSUGA_PATENTES NA -QFMT=fastap -SUFFIX=p2n.rni--MINMATCH=0.1 -LGOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LCGAL -OUTFWT=PETC -NORM=ext -HEARSIZE=500 -MINIMENEO -MAXLEN=200000000
-USER=LOCAL-OUTFWT=PETC -NORM=ext -HEARSIZE=SOO -MINIMENEO -NORUGE -ICPU=3
-NO NMAP -LARGEQUERY -NGG SCORRES - WALT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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34, Appli
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37, Appl
12, Appl
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                                                                                           August 17, 2003, 19:49:34; Search time 57.7778 Seconds (without alignments) 1405.636 Million cell updates/sec
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Sequence 37,
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US-09-206-059-30
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US-09-775-325-3
US-09-561-500-12
US-09-561-108-12
US-09-561-56-12
US-09-561-108-12
US-09-561-108-12
US-09-561-108-12
US-09-561-499-12
US-08-159-784-1
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              GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArglle 100
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                                                       ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
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APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER RADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/159,784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US
FILING DATE: December
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3394
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STATE: Massachusetts
COUNTRY: U.S.A.
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STRANDEDNESS: single
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US-08-159-784-4
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Use
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                   GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
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Mismatches:
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Fatent No. 6201104
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Anadiogenesis Inhibiting Profile OF INVENTION: Anadiogenesis Inhibiting Profile OF INVENTION: Proteins and Methods of Use; FILE REFERENCE: 05213-0370
CURRENT APPLICATION NUWBER: US/09/206,059; CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.0
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85.08%
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, ORGANISM: Homo sapiens
US-09-206-059-30
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; ORGANISM: Rattus rattus US-09-449-293-3
                                                 Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                Alignment Scores:
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; Sequence 3, Application US/09449293
; Patent No. 626/954
; GENERAL INFORMATION:
APPLICANT: Ablibol, Marc
; APPLICANT: Wene ack, Maurice
APPLICANT: Bossard, Carine
APPLICANT: Bossard, Carine
APPLICANT: Bonnel, Sebastion
APPLICANT: Bonnel, Sebastion
APPLICANT: Honiger, Jiri
APPLICANT: Prats, Herve
APPLICANT: Neuner-Jehle, Martin
TITLE OF INVENTION: INTRACULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 80766.2020501
CURRENT APPLICANTON NUMBER: US/09/449,293
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
LENGTH: 558
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                                                                                                     HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro
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           3394
154
14
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           Length:
Matches:
Conservative:
Mismatches:
                                                                                 US-09-938-391-4 (1-184) x US-08-159-784-4 (1-3394)
                                                  Indels:
                                                               Gaps:
         1.26e-86
835.00
92.82%
85.08%
86.44%
                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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 Alignment Scores:
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US-09-449-293-3
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APPLICANT: Honiger, Jiri
APPLICANT: Neuner-Jehle, Martin
TITLE OF INVENTION: INTRAOCCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.202USD1
CURRENT APPLICATION NUMBER: US 09/775,325
PRIOR APPLICATION NUMBER: US 09/449,293
PRIOR FILING DATE: 1999-11-24
558
154
17
13
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                    US-09-938-391-4 (1-184) x US-09-449-293-3 (1-558)
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APPLICANT: Uteza, Yves
APPLICANT: Menasche, Maurice
APPLICANT: Bossard, Carine
APPLICANT: Van Den Berghe, Loic
APPLICANT: Bonnel, Sebastian
APPLICANT: Prats, Herve
2.23e-87
831.00
92.93%
83.70%
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92.93%
83.70%
86.02%
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Best Local Similarity:
Query Match:
 U.S.A.
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TOPOLOGY: 11
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Pred. No.:
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 COUNTRY:
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Patent No. 6080728
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
THERAPY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
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Gaps:
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1220 Market Street, P.O. Box 2207
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         SOFTWARE: Patentin version
SEQ ID NO 3
LENGTH: 558
                                              TYPE: DNA ORGANISM: Rattus
NUMBER OF SEQ ID NOS:
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Best Local Similarity:
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STREET: 122
CITY: Wilmi
STATE: Dela
                                                                                            Alignment Scores:
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US-08-985-526-37
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Mismatches:
Indels:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/608,845
FILING DATE:
FRIOM APPLICATION DATA:
APPLICATION NUMBER: US/08/608,845
FILING DATE:
FLING NAME: US/08/608,845
TELEPHONE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (302) 658-541
TELEPHONE: (302) 658-541
TELEPHONE: (302) 658-5613
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: S65 base pairs
TYPE: nucleic acid
STYPE: nucleic acid
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Matches:
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; Sequence 12, Application US/09561108
; Patent No. 6342221
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; LOCATION: (1)..(573)
US-09-561-108-12
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                RESULT 7

US-09-561-500-12

US-09-561-500

Sequence 12, Application US/09561500

Patent No. 634219

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe

APPLICANT: ROLf A. Brekken

TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF

FILE REFREENCE: 4001.025200

CURRENT APPLICATION NUMBER: US/09/561,500

CURRENT PILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR FILING DATE: 1999-04-28
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OTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEY: CDS
1. LOCATION: (1)..(573)
US-09-561-500-12
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ORGANISM: Artificial Sequence
FEATURE:
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92.93%
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SerPheSerLys 184
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SOFTWARE: Patentin Vel
SEQ ID NO 12
LENGTH: 573
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Best Local Similarity:
Query Match:
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GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
IITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: 05/9/561,108
CURRENT FILING DATE: 2000-04-28
FILM PAPLICATION NUMBER: 60/131,432
FRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PALENTIN Ver: 2.0
SEQ ID NO 12
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TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: OLIGONUCLEOTIDE
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                  GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 160
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Sequence 12, Application US/09561499

Sequence 12, Papplication US/09561499

Sequence 12, Papplication US/09561499

Sequence 12, Papplication US/09561499

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Philip E. Thorpe

TILE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

FILE REPERENCE: 4001.002582

CURRENT APPLICATION NUMBER: US/09/561,499

CURRENT PILING DATE: 2000-04-28

PRIOR FILING DATE: 1999-04-28
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ORGANICAH: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: OLIGONUCLEOTIDE
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 573
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; LOCATION: (1)..(573)
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OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
OTHER INFORMATION: OLIGONUCLECTIDE
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US-09-561-526-12

Sequence 12, Application US/09561526

Patent No. 6416758

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR
FILE REFERENCE: 4001.002586

CURRENT APPLICATION NUMBER: US/09/561,526

CURRENT FILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 12

LENGTH: 573
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ORGANISM: Artificial Sequence
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; LOCATION: (1)..(573)
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 GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla 40
                                                                                                                                            ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
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                                                                       GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
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Patent No. 6146510
BERERAL INFORMATION:
APPLICANT: Folkman, Judah
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REPERENCE: 05213-0229
CURRENT APPLICATION NUMBE: 1999-05-20
CURRENT FILING DATE: 1999-05-20
SOUTHWARE: Patentin Ver. 2.0
SEQ. ID NO 6
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; ORGANISM: Homo sapiens
US-09-315-689-6
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                    141 GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln
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HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
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Patent No. 5643783
GENERAL INFORMATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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Mismatches:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
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NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0024f
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Fish & Richardson
225 Franklin Street
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ATTORNEY/AGENT INFORMATION:
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4031
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: Massachusetts
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	RESULT 14  US-09-252-991A-15284/C  i Sequence 15284, Application US/09252991A  Pacent No. 6551795  GENERAL INFORMATION:  APPLICANT: Warc J. Rubenfield et al.  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  FILE REFERENCE: 107196.136  CURRENT APPLICATION NUMBER: US 60/074,788  PRIOR PELING DATE: 1999-02-18  PRIOR APPLICATION NUMBER: US 60/094,190  SEQ ID NO 15284  LENGTH: 2319  TYPE: DNA  CORGANISM: Pseudomonas aeruginosa  US-09-252-991A-15284	Alignment Scores: Pred. No.: Scores: Pred. No.: Scores: 90.50 Matches: 55 Percent Similarity: 38.71% Conservative: 17 Best Local Similarity: 29.57% Mismatches: 62 Query Match: 4 Indels: 53 Best Local Similarity: 29.57% Mismatches: 62 Query Match: 4 Indels: 53 Best Local Similarity: 19.37% Mismatches: 62 Gaps: 08-09-938-391-4 (1-184) x US-09-252-991A-15284 (1-2319)  Qy 18 ProGlnProGlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAla 37
0y         45 ThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerlleValArgArgAla 64           121 ACCTTCGGGGCTTCCTGGCGCCTGCAGGACCTGTACAGCATCGTGGCGCGTGCC           0y         65 AspArgThrGlyValProValValAsnLeuArgAspGluValLeuPheProSerTrpGlu 84           181 GACCGCGAGCCGTGCCAACCTCAAGGACGAGCTGCTGTTTGCL 180           0y         85 AlaLeuPheSerGlySerGluGlyGlnLeuLySProGlyAlaArgllePheSerPheAsp 104           19	SULT 13 SULT 145455 Sequence 15455, Application US/09252991A Patent No. 6551795 SAPELOCANT: MAC J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATITLE OF INVENTION: NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US 60/094,788 PRIOR PELING DATE: 1999-02-18 PRIOR PELING DATE: 1999-02-18 PRIOR FILING DATE: 1999-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 15455 LENGTH: 591 TYPE: DNA ORGANISM: Pseudomonas aeruginosa	A  Q  A  Q  A  Q  B  C  G  G  G  G  G  G  G  G  G

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 10196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
SEQ ID NO 15396
LENGTH: 2427
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   1594 CGGTTTCGCTTTCGACCGGCAGCAGCGCGCCAGGTCGAGGCGCAGGTCGCGTTCCCCGGT 1535
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              83
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74 LeuArgAspGluValLeuPheProSerTrpGluAlaLeuPheSer-
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Search completed: August 17, 2003, 23:00:11 Job time : 62.7778 secs THIS PAGE BLANK (USPTO)

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Sequence 37, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 2, Appli
Sequence 5, Appli
Sequence 59, Appl
Sequence 159, Appl
Sequence 64, Appl
Sequence 7650, Ap
Sequence 1, Appli
Sequence 113, Appli
Sequence 2569, Ap
                                          Sequence 4, Appli
Sequence 3, Appli
Sequence 53, Appl
Sequence 30, Appl
Sequence 2178, Ap
Sequence 144, App
Sequence 48, Appl
Sequence 3, Appli
Sequence 3, Appli
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APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Lo, Kin-Ming
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
FILE REPRENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENTH: SS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Appl
Sequence 5, Appli
Sequence 16, Appli
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Sequence 3816, Ap
Sequence 2071, Ap
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Seguence 309, Apr
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14 US-10-131-241-50

14 US-10-31-241-51

14 US-10-22-418-3

12 US-10-292-418-3

13 US-09-880-107-2178

14 US-10-131-241-48

15 US-09-775-174-48

16 US-09-775-174-3

17 US-10-98-831-12

18 US-09-775-174-3

19 US-09-775-174-3

10 US-09-998-831-12

11 US-10-99-81-15-9

12 US-10-99-81-15-9

14 US-10-131-241-45

15 US-10-080-797-4

16 US-10-131-241-45

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18 US-10-131-241-45

19 US-10-131-241-45

10 US-10-131-241-45

11 US-10-060-036-4

12 US-10-080-797-4

13 US-10-131-241-45

14 US-10-131-241-45

15 US-09-917-392-159

16 US-10-15-650-036-4

17 US-10-15-632-976-33
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US-09-815-981-5
US-09-815-911A-16
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US-10-225-567A-309
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Publication No. US20030139365A1
GENERAL INFORMATION:
        1344 9025608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Canis familiaris FEATURE: NAME/KEY: CDS
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/CgnZ_1/USFTO_spool p/US09938391/runat_04082003_1130658_27206/app_query.fasta_1.718
-Q=/CgnZ_1/USFTO_spool p/US09938391/runat_04082003_1130658_27206/app_query.fasta_1.718
-DE-Published Applications NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOÖPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR MXX=EDCT -THR MXX=10
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-NCPU=6 -ICPA=3 -NO MMAP -LARGEQUERY NEG SCORES=0 -WAIT -DSPBALCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Appl
                                                                                                                                        August 17, 2003, 21:56:45 ; Search time 215.556 Seconds (without alignments) 1910.324 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
                           GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                        OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 12 US-10-292-418-34
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Perfect score:
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Sequence 51, Application US/10131241
| Publication No. US20030012792A1
| Publication No. US20030012792A1
| GENERAL INFORMATION:
| APPLICANT: Holaday, John W. APPLICANT: Fortier, Anne H. TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifers
| TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifers
| TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
| FILE REFERENCE: 05213-0344 43170-271565 | CURRENT APPLICATION NUMBER: US/310/131,241 |
| CURRENT APPLICATION NUMBER: US 09/413,049 |
| PRIOR FILING DATE: 1999-10-06 |
| PRIOR FILING DATE: 1999-05-21
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                ; TYPE: DNA
; ORGANISM: Canine
US-10-131-241-50
SOFTWARE: Pate
SEQ ID NO 50
LENGTH: 552
                                                                                                                    Alignment Scores:
Pred. No.:
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US-10-131-241-51
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Sequence 50, Application US/10131241

Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: US 2002-07-22

FILE REFRENCE: 05213-034 41170-271565

CURRENT APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 65
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Matches:
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Mismatches:
Indels:
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                                                                                                                                                                     Gaps:
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 ; LOCATION: (1)..(552)
; OTHER INFORMATION: Endostatin
US-10-292-418-34
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Best Local Similarity:
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Pred. No.:
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                       CURRENT APPLICATION NUMBER: US 05/10/042,347
CURRENT FILING DATE: 2002-01-11
PRIOR FILING DATE: 2002-01-11
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR PILING DATE: 1998-09-16
PRIOR PILICATION NUMBER: US 09/154,302
PRIOR PELICATION NUMBER: US 09/154,302
PRIOR PELICATION NUMBER: US 09/154,302
PRIOR PELICATION NUMBER: US 08/740,168
PRIOR PILING DATE: 1996-10-22
PRIOR PILING DATE: 1996-10-22
PRIOR PILING DATE: 1996-02
PRIOR PILING DATE: 1996-02
PRIOR PILING DATE: 1996-02
PRIOR PILING DATE: 1996-02
PRIOR PILING DATE: 1996-09-02
PRIOR PILING DATE: 1996-09-02
PRIOR PILING DATE: 1996-09-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PARCENTIN VERSION 3.1
SEQ ID NO 9:
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               FILE REFERENCE: 05213-0880 (43170-249874)
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835.00
92.82$
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Query Match:
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Publication No. US20030114370A1
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael S.
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Endostatin Protein and Peptide
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 CGTGCGCCGTGCTGACCGGGGGTCTGTGCCCATCGTCAACCTGAAGGACGAGGTGCTATC 239
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                                                                                                                                                                                           Length:
Matches:
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51
LENGTH: 632
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891.00
84.83*
83.89*
92.24*
                                                                                                          ; TYPE: DNA
; ORGANISM: Murinae sp.
US-10-131-241-51
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Best Local Similarity:
Query Match:
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141 GlualaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 160
161 GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 180
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                             CARREAT INVOCATION:

APPLICANT: Li, Yue, Stephen D
APPLICANT: Li, Yue, Stephen D
APPLICANT: Li, Yue, Stephen D
TITLE OF INVENTION: Expression and Export of
TITLE OF INVENTION: Immunofusins
FILE REFERENCE: LEX-OOGCI
CURRENT PEPLICATION NUMBER: US/O/292,418
CURRENT FILING DATE: 2002-11-12
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver: 2.0
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                                              Sequence 3, Application US/10292418
Publication No. US20030139365A1
GENERAL INFORMATION:
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OTHER INFORMATION: endostatin
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835.00
92.82%
85.08%
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
GCC 543
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LOCATION: (1)
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                     RESULT 5
US-10-292-418-3
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US-10-131-14

US-10-14-141-53

US-10-14-141-14

US-10-14-14-14

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US-10-14-14-14

US-10-14-14-14

US-10-14-14-14

US-10-14-14-14

US-10-14-14-14

US-10-14-14-153

US-10-131-24-1-53 140 240 81 ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArgile 100 300 360 420 540 101 PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 120 121 GGGCTGGCGGCGCCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180 9 80 40 241 CCCAGCTGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGCACGCATC HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro 21 GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla 61 ValargargalaaspargThrGlyValProValValAsnLeuArgaspGluValLeuPhe. 121 HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr 41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerlle 

us-09-938-391-4.p2n.rnpb

	Oy 161 GlualaalaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 180	Qy 181 Ser 181 1:: Db 541 GCC 543	RESULT 8  US-09-880-107-2178  Sequence 2178, Application US/09880107  Patent No. US20020142981A1  GENERAL IMPORMATION:  APPLICANT: Horne, Darci T.  APPLICANT: Vockley, Joseph G.  APPLICANT: Gene Logic, Inc.  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer; FILE REFERENCE: 44921-5028-W0  CURRENT APPLICATION NUMBER: US 60/211,379  PRIOR PRIOR APPLICATION NUMBER: US 60/211,379  PRIOR PRIOR PLING DATE: 2000-06-14  PRIOR PRIOR FILING DATE: 2000-06-14  PRIOR PRIOR PRIOR DATE: 2000-06-14  PRIOR FILING DATE: 2000-06-16  NUMBER OF SEQ ID NOS: 3950  SOFTWARE: PATENTIN VERICALION OF SEQ ID NOS: 3950  SUBJURIED DATE: 2000-10-10  SUBJURIED DATE: 2000-10	ORMATION: 0 -2178 res: arity: milarity:	05-03-338-391-4 (1-184) X 05-09-880-107-2178 (1-3394)  Qy	Qy 21 GlyGlyMetArgGlylleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla 40	Oy	Qy 61 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe 80	Qy 81 ProSerTrpGluAlaLeuPheSerGluGluGluGluGluGluGluGluGluGluGluGluGluG	Qy	Ov 121 HisGlvSerAspProSerGlvArgArgLeuThrAspSerTvrCvsGluThrTrpArgThr 140
	Qy 161 GlualaalaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 180	Qy 181 Ser 181 ::: Db 541 GCC 543	pplication US/09873676 0020077289A1 ATTON: CDOnald, Nicholas J. Im, Kim L. The Majostatin and Endostatin Binding Proteins and Methods E: 05213-0378 (43170-259333) CATION NUMBER: US/09/873,676 DATE: 2001-06-02 TION NUMBER: US 60/209,065 DATE: 2000-06-02 TION NUMBER: US 60/289,387 DATE: 2010-05-08 TON NUMBER: US 60/289,387			Oy 41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 60	Oy 61 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe 80	Qy         81 ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLySProGlyAlaArgIle 100           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         101 PheserPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 120	Oy 121 HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr 140	Qy 141 GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGlu 160

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121 HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr 140
                                                             141 GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 160
                                                                                                                        161 GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 180
                   4360 CATGGCTCGGACCCCAACGGCGCAGGCTGACCGAGAGCTACTGTGAGACGTGGCGGACG
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                                            4000 CACAGCCACCGGGATTCCAGCCGGTGCTCCACCTGGTTGCGCTCAACAGCCCCCTGTCA 4059
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JAPPLICANT: Benson, Darin R.
JAPPLICANT: Kalos, Michael D.
JAPPLICANT: Alos, Michael J.
JAPPLICANT: Peresing, David H.
JAPPLICANT: Hepler, William T.
JAPPLICANT: Hepler, William T.
JAPPLICANT: Jang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
JOHN PROBLEM FOR SEQ FOR WINDOWS VERSION 4.0
JOHN PROBLEM FOR SEQ FOR WINDOWS VERSION 4.0
JENGTH: 4551
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Matches:
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                                                                                                                                                                                                                                                            Sequence 144, Application US/10060036; Publication No. US20030073144A1; GENERAL INFORMATION:
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835.00
92.82%
85.08%
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ORGANISM: Homo sapiens
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Query Match:
DB:
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2044 GCC 2046
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Percent Similarity:
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RESULT 10 US-10-131-241-48 ; Sequence 48, App ; Sequence 48, App ; Publication No. ; GRNERAL INPORMA- ; APPLICANT: HOLANT: HOLANT: HOLANT: HOLANT: HOLANT: PRICHENCE CURRENT FILING PRIOR APPLICATION PRIOR FILING DIPRIOR FILING FILIN	-241-46 e 48, information in the control of the con	SULT 10 -10-131-241-48 -10-131-241-48 Publication No. US20030012792A1 GENERAL INPORMATION: APPLICANT: Holaday, John W. APPLICANT: Fortier, Anne H. TITLE OF INVENTION: Compositions TITLE OF INVENTION: and Regulat FILLE REPERENCE: 05213-034 4 317 CURRENT APPLICATION NUMBER: US 09/PRIOR APPLICATION NUMBER: US 09/PRIOR FILING DATE: 1999-10-06 PRIOR APPLICATION NUMBER: US 09/PRIOR FILING DATE: 1999-05-21 PRIOR FILING DATE: 1999-05-22 PRIOR FILING DATE: 1999-05-22 PRIOR FILING DATE: 1999-05-22 RIOR APPLICATION NUMBER: US 60/PRIOR FILING DATE: 1998-05-22 BRIOR FILING DATE: 1998-05-22 BRIOR FILING DATE: 1998-05-22 BRIOR FILING DATE: 1998-05-22 BRIOR FILING DATE: 1998-05-22 COFTWARE: PALENTIN VERSION 3.1 LENGTH: 540 TYPE: DNA ORGANISM: Rhesus monkey	lication US/101 US20030012792A1 TON: day, John W. tier, Anne H. TON: Compositio USA: 3034 43 USA: 3034 43 USA: 2002-07- CON NUMBER: US O ON NUMBER: US O TE: 1999-06-21 ON NUMBER: US O TE: 1999-05-22 D NOS: 65 III version 3.1	SULT 10 -10-131-241-48 Sequence 48, Application US/10131241 Sequence 48, Application US/10131241 Sequence 48, Application US/10131241 GENERAL INFORMATION: APPLICANT: Holaday, John W. APPLICANT: Fortier, Ann W. TITLE OF INVENTION: Compositions and Me FILE REFERENCE: 05213-0344 43170-27156 CURRENT APPLICATION WUMBER: US 09/413,049 PRIOR APPLICATION WUMBER: US 09/413,049 PRIOR FILING DATE: 1999-05-21 PRIOR FILING DATE: 1999-05-21 PRIOR FILING DATE: 1999-05-21 PRIOR FILING DATE: 1999-05-21 RIGHT APPLICATION NUMBER: US 60/086,586 PRIOR APPLICATION NUMBER: US 60/086,586 PRIOR FILING DATE: 1999-05-22 NUMBER OF SEQ ID NOS: 65 SOFTWARE: PatentIN version 3.1 LENGTH: 540 LTYPE: DNA ORGANISM: Rhesus monkey	10-131-241-48  10-131-241-48  equence 48, Application US/10131241  ublication No. US20030012792A1  ENERAL INPORMATION: APPLICANT: Holaday, John W. APPLICANT: Fortier, Anne H. TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: and Regulating Angiogenesis FILE REFERENCE: 05213-0344 43170-271565  CURRENT APPLICATION NUMBER: US/10/131,241  CURRENT FILING DATE: 1999-10-06  PRIOR FILING DATE: 1999-10-06  PRIOR FILING DATE: 1999-10-06  PRIOR FILING DATE: 1999-10-20  PRIOR APPLICATION NUMBER: US 60/086,586  PRIOR APPLICATION NUMBER: US 60/086,586  PRIOR FILING DATE: 1998-05-21  PRIOR FILING DATE: 1998-05-22  NUMBER OF SEQ ID NOS: 65  SOFTWARE: PATENTIN VERSION 3.1  LENGTH: 540  TYPE: DNA  ORGANISM: Rhesus monkey		ng Cano	Inhibiting Endothelial Using Cancer Markers	Ce11	Prolifer	
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:	Scor: imila l Sim	res: urity: nilarity:	7.35e-9831.00 92.22\$ 84.44\$ 86.02\$	e - 93 28 48 28	Length: Matches: Conservative Mismatches: Indels: Gaps:	**	540 152 14 0				
US-09-938	-938-391-4	-4 (1-184)		x US-10-131-241	-241-48 (1-540)						
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ço qa	21	GlyGlyMe          GGCGGCAT	tArgG1        GCGGGGG	yllearggly <sup>2</sup>                Calccgcggg	GlyGlyMetargGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla 	ysPhe      GCTT	egingin         ccagcag	Alaargalaala           GCACGGCCGTG	1 40		
& ସ	41	GlyLeuAl         GGGCTGGT	aGlyTh       GGGCAC	rPheArgAlaE            CTTCCGTGCCT	GlyLeualaglyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 	rgle       GGCT(	IGInAsp         3CAGGAC	LeuTyrSerlle	60		
ço, qa	61	ValArgAr          GTGCGCCG	galaas        TGCCGA	pargthrGlyV       cccccacccc	ValArgArgAlaAspArgThrG1yValProValValAsnLeuArgAspG1uValLeuPhe 	snLet      ACCT	Argasp  :::     AAGGAT	GluValLeuPhe     :::        GAGCTGCTGTTT	240		
Qy Dp	81	ProSerTr          CCCAGCTG	pglual        GGAGGC	GluAlaLeuPheSerGl;                gaGGCTTTGTTCGCAGG	ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLySProGlyAlaArgIle 	InLe  -  -  -	JLYSPro          SAAGCCC	GlyAlaArgile 	100		
ò	101	PheSerPh	eAspGl	yArgAspVall	$\tt Phe SerPhe AspGly Arg AspValLeuGln HisProAlaTrpProArgLysSerValTrpProBroArgLysSerValTrpPro$	laTri	pProArg	LysSerValTr	120		

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141 GluAlaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 160
                                                                                                                                                                                                                                                                                                                   161 GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 180
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     101 PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 120
                                                                                                                                                                                                                                             21 GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
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                              304 TITICITITIGACGGCAGAGATGTCCTGAGACACCCAGCCTGGCCGCAGAAGAGCGTATGG
                                                                                                      121 HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
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APPLICANT: Honiger, Jiri
APPLICANT: Neuner-Jehle, Martin
TITLE OF INVENTION: INTRACOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.2020501
CURRENT APPLICATION NUMBER: US/09/775,325
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: US 09/449,293
PRIOR FILING DATE: 1999-11-24
SOFTWARE: PATENTING PATE: 1999-11-24
SOFTWARE: PATENTING PATE: 1999-11-24
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Patent No. US20020076397A1
GENERAL INFORMATION:
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APPLICANT: Menasche, Maurice
APPLICANT: Bossard, Carine
APPLICANT: Wan Den Berghe, Loic
APPLICANT: Bonnel, Sebastian
APPLICANT: Prats, Herve
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Query Match:
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301 TTCTCCTTTGACGGCAAGGACGTCCTGAGGCACCCCCACTGGCCCCAGAAGAGGGCGTGTGG 360
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                                                                             HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr 140
                                                                                                           361 CATGGCTCGGACCCCAGCGGGCGCGAGGCTGACTGAGAGCTACTGCGAGACGTGGCGGACA 420
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APPLICANT: Neuner-Jehle, Martin
ATILLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.2020208
CURRENT APPLICATION NUMBER: US/09/775,174
PRIOR APPLICATION NUMBER: US/09/775,175
PRIOR PLING DATE: 1999-11-24
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Patent No. US20020076396A1
GENERAL INFORMATION:
APPLICANT: Abitbol, Marc
APPLICANT: Uteza, Yves
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Bossard, Carine
Van Den Berghe, Loic
Bonnel, Sebastian
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SOFWARE: Patentin version 3.1
SEQ ID NO 558
LENGTH: 558
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US-09-775-174-3
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Pred. No.:
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US-09-775-174-3
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APPLICANT:
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Percent Similarity: 92.93% . Conservative: 17 Best Local Similarity: 83.70% Mismatches: 13 Query Match: 86.02% Indels: 0 DB: 13	US-09-938-391-4 (1-184) x US-10-036-869-37 (1-565)	1 HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro	DD 11 CAIACICAICAGACTTICAGCCAGTGCTCCACCTGGTGGGCACTGAACACCCCCTGGTC7 70  21 G1YG1YMGCAATGG1YTIGATGG1YALAASDPheG1nCJTAGAATAGAATAAAAA 40	Db 71 GGAGGCATGCGTGGTATCCGTGGAGCTGTCCAGTGCTACCAGGCCGTG 130	Oy 41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSer11e 60	Oy 61 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe 80	81 ProserTrpGluhlaLeuPhescelluGlyGlnLeuLysProGlyAlaArglle	Db 251 CCCAGCTGGGACTCCCTGTTTTCTGGCTCCCAGGGTCAACTGCAACCGGGGCCCGCATC 310	Qy 101 PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 120	Oy 121 HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr 140	Oy 141 GlualaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 160	Qy         161 GlublaAlaSerCysArgHisAlaPheValValLeuCysIleGlubsnSerValMetThr 180           :::                         bb         491 AAAGCTGCCACAACAACACTACATCCTCCTGTGCATTGAGATAGCTTCATGACC 550	181 SerPheSerLys 184	Db 551 TCTTTCTCCAAA 562	RESULT 14 US-09-98-831-12	; Sequence 12, Application OS/05990531 ; Patent No. US20020119153A1 ; GENERAL INFORMATION:	,	; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY ; TITLE OF INVENTION: INHIBITING VEGF ; FILE REFERENCE: 4001.002684	; CURRENT APPLICATION NUMBER: US/09/998,831 ; CURRENT FILING DATE: 2001-11-30	; PRIOR APPLICATION NOMBER: 09/561,108 ; PRIOR FILING DATE: 2000-04-28 ; NUMBER OF SEQ ID NOS: 44	; SoFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 12 ; LENGTH: 573	1 Sequence	; OTHER INFORMATION: Description of Artificial Sequence: SYNTHEFIC ; OTHER INFORMATION: OLIGONUCLEOTIDE ; NAMP/FEV. CHE	invigival: (1) (573) i LoCATION: (1) (573) US-09-998-831-12
Oy 81 ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArgIle 100	Oy 101 PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 120	304 TTTCTTTTGACGGCAGAGATGTCCTGAGACACCCAGCCTGGCCGCAGAGAGGGGTATGG	OY 121 HISAYSerasperosesty.Magatgleulnraspersycysturinripaginr 140  121 HISASPEROSESTYSERS	Qy         141 GlualaProAlaAlaThrGlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGln 160	Db 424 GAAACTACTGGGGCTACAGGTCCTCCTCCTGCTGTGTGTCTCTGGAACTG 483  Qy 161 GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 180	Db 484 AAAGCTGCGAGCFGCCACAACAGCTACATCGTCCTGTGCATTGAGAATAGCTTCATGACC 543 Ov 181 SerPheSerIvs 184	544 TCTTTCTCCAAA	RESULT 13 US-10-036-869-37	Sequenc Publica GENER	; APPLICANT: Mixson, James A . ; TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA . ;; THERAPY THERAPY .	; NUMBER OF SEQUENCES: 43 ; CORRESPONDENCE ADDRESS: ; STREET: 1220 Market Street, P.O. Box 2207	; CITY: Wilmington ; STATE: Delaware ; CUUNTRY: U.S.A. ; ZTP: 19899	COMPUTER READABLE FORM:	COMPUTER: IBM PC compatible COMPATION SYSTEM: PC-DOS/MS-DOS COMPANE: PatentIn Release #1.07		; FILING DAIE: Z9-WO. USZUUZUISISADI-ZUUI ; CLASSIFICATION: «Unknown» : PRIOR APPLICATION DATA:	APPLICATION NUMBER: US/08/985,526; FILING DATE: <unknown></unknown>	; APPLICATION NUMBER: US 08/608,845 ; FILING DATE: 16-UL-1996 . ATTONEY AGENT INFORMATION:	g g	; TELEFAX: (302) 658-9141 ; INFORMATION FOR SEQ ID NO: 37:	; SEQUENCE CHARACTERISTICS: ; LENGTH: 565 base pairs ; TYPE: nucleic acid	; STRANDEDNESS: single ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 37:	US-10-036-869-37	Arigiment Scores: 7.78e-93 Length: 565 Score: 831.00 Matches: 154

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82 GGAGGCATGCGTGTATCCGTGGAGCAGATTTCCAGTGCTTCCAGCAAGCCCGAGCCGTG 141
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Publication No. US20030139365A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of
TITLE OF INVENTION: Immunotisins
FILE REFERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT PILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
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Job time : 224.556 secs
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) ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(552)

; OTHER INFORMATION: endos

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

August 17, 2003, 19:46:50 ; Search time 1630.67 Seconds (without alignments) 2742.451 Million cell updates/sec US-09-938-391-4 966 1 HTHQDFQLVLHLVALNSPQP.......CRHAFVVLCIENSVMTSFSK 184 Title: Perfect score: Sequence: Scoring table: Run on:

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22781392 seqs, 12152238056 residues Searched:

45562784 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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RESULT 1 BE908201

BE908201 707 bp mRNA linear EST 20-OCT-2000 001500458F1 NIH\_MGC\_70 Homo sapiens cDNA clone IMAGE:3902175 5', Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 707) BE908201.1 GI:10402537 Homo sapiens (human) Homo sapiens mRNA sequence. BE90820 EST. VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION ACCESSION

REFERENCE

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
LLAM970 prow: i column: 09
High quality sequence stop: 757.
Plate: LLAM970 prow: i column: 09
High quality sequence stop: 757.

Location/Qualifiers
I.: 757.

Amol_type="mRNA"

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1 (bases 1 to 757)
11 hMG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9704 row: d column: 16
High quality sequence stop: 688.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
Conservative:
Mismatches:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/mol_type="mRNA"

/db_txef="txef="txen:9606"

/clone="type="Pituitary"

/lab_host="DH10B-Tron A (T1 and T5 phage resistances)"

/lab_host="DH10B-Tron A (T1 and T5 phage resistances)"

/clone=llb="NIH MGC 179"

/clone=llb="NIH MGC 179"

/clone=llogan: brain; Vector: pcMV-SPORT6.1; Site 1: EcoRV

/destroyed); Site_2: Not1; Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon cloning

). Average insert size 1.1 kb. Library was constructed by

(Invitrogen). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                               CD105862 881 bp mRNA linear EST 15-MAY-2003
AGENCOURT_14021788 NIH_MGC_179 Homo sapiens cDNA clone
IMAGE:30365831 5', mRNA sequence.
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                                                                                                    PheSerPheAspGlyArgAspValleuGlnHisProAlaTrpProArgLysSerValTrp 120
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NIH-WGC http://mgc.nci.nih.gov/.
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Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone through the I.M.A.G.E. Consortium/Link at:
http://image.lln.gov
plate: NDAM424 row: g column: 24
High quality sequence stop: 689.
ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArgIle
                                                             CCCAGCTGGGGAGGCTCTGTTCTCAGGCTCTGAGGGTCCGCTGAAGCCCGGGGGCACGCATC
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Length:

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602046021F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4195660 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 843)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lefound through the I.M.A.G.E. Consortium/LLNL)
thtp://image.llnl.gov
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Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
57 a 278 c 228 g 170 t
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60299046вF1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5146409 5',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 CATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTGGCACTGAACACCCCCCTGTCT 230
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                                                                                                                                                                                                                                                                                                                                                                                                                               1 HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro 20
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117
117
0
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                   FEATURES
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DEFINITION

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bentco Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11361 row: g column: 18
High quality sequence start: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322
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                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 874)
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                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                               Unpublished
Contact: Robert Strausberg, Ph.D.
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Mus musculus (house mouse)
Mus musculus
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81 ProserTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArg11e 100	
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GlualaProalaalaThrGlyGlnalaSerSerLeuLeualaGlyargLeuLeuGluGlu 	
GlualaalaserCysargHisalaPheValValLeuCysIleGluAsnSerValMetThr 180 :::             aaaGcrGcGGAGCrGcCaCaaCaGCTACATCGTCCTGTGCATTGAGAATAGCTTCATGACC 682	t 6 4 6
PheserLye 184           TTCTCCAA 694	
CBS96713 715 bp mRNA linear EST 03-APR-2003 AGENCOURT 12990486 NIH MGC 178 Mus musculus cDNA clone IMAGE:30299651 5', mRNA sequence.	Oy 82 SerTrpGluAlaLeuP)  Oy 82 SerTrpGluAlaLeuP)  Db 245 AGCTGGGACTCCCTGT  Oy 102 SerPheAspGlyArgA
CB596713.1 GI:29514569 BST. Mus musculus (house mouse) Mus musculus Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	305
	1 4 2 4 4 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Michael Brownstein CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bloscience Corporation Clone distribution: MGC clone distribution information can be	162 162 485 182
round through the 1.M.A.G.E. Consortium/LENL at: http://image.llnl.gov column: 12 hide: NDCM64 row: b column: 12 High quality sequence stop: 567. Location/Qualifiers 1715 /organism="Mus musculus"	RESULT 7  RESULT 7  REO74459  LOCUS  DEFINITION 221883 MARC 2BOV ACCESSION BF074459
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	Keele, J.W. Sequence evalua
51 a 205 c 201 g 158 t	JOURNAL Genome Res. 11 (4) MEDLINE 21180013 PUBMED 11282978

Alignment Scores:

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EST 25-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                       GlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThrGlu 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., E., White, J., Cho, J., Fahrenkrug, S.C., Bennett P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                ArgalaPheLeuSerSerArgLeuGlnAspLeuTyrSerlleVal 61
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                                                                                                               551 bp mRNA linear
Bos taurus cDNA 5', mRNA sequence
  715
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                        96713 (1-715)
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Contact: Smith TPL
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COMMENT
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Cuther ESTS: ura3h10.x1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml
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Site_2: NOtI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
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Indels:
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Location/Qualifiers
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                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                                                   AW911243
AW911243.1 GI:8076490
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Query Match:
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ORIGIN
                                                                           DEFINITION
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TITLE
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                   RESULT 8
AW911243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaSerSerLeuLeuAlaGlyArgLeuLeuGluGluGluAlaAlaSerCygArgHisAla 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlySerGluGlyGlnLeuLysProGlyAlaArgllePheSerPheAspGlyArgAspVal 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGlnHisProAlaTrpProArgLysSerValTrpHisGlySerAspProSerGlyArg 128
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                                                                                         Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.

PCR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

        AlaAspPheGlnCysPheGlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAla

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GGCTCCGAGGCCCAGCTGAAGCCCGGCGCCCGCATCTTCTCCTTCGACGCCAGAGGTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheValValLeuCysIleGluAsnSerValMetThrSerPheSerLys 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551
157
9
10
0
USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 1830 Email: smith@engail.marc.usda.gov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 81 row: F column: 9
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-938-391-4 (1-184) x BF074459 (1-551)
                                                                                                                                                                                                                                                    Location/Qualifiers
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822.00
94.32%
89.20%
85.09%
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Best Local Similarity:
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602877005F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5008608 5', BI080524
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 228 c 205 g 166 t
                                                                                                                                                                                                                                                                                                                          CATACTCATCAGGACTTTCAGCCAGTGCTCCACCTGGTGGCACTGAACACCCCCCTGTCT 122
                                                                                                                                                                                                                                                                                                                                                                                            GGAGGCATGCGTGGTATCCGTGGAGATTTCCAGTGCTTCCAGCAAGCCCGAGCCGTG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 897)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                       HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro
                                                                                                                                                                                                                                                                                                                                                                       GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 TTTCTTTGACGGCAGAGATGTCCTGAGACACCCCAGCCTGGCCGCAGAAGAGCGTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
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                                                                                                                                                       753
154
16
11
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                   8.19e-69
806.00
92.39%
83.70%
83.44%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMILGAR row: e column: 03
High quality sequence start: 31
High quality sequence start: 51.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B1904605 753 bp mRNA linear EST 16-OCT-2001 603168411F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5256554 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 753)
                   80
                 ValArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhe
                                                                               ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeulysProGlyAlaArgIle
                                                                                                    CCCAGCTGGGACTCCCTGTTTTTCTGGCTCCCAGGGTCAACTGCAACCCGGGGCCCGCATC
                                                                                                                                                PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp
                                                                                                                                                                     TITICITITIAGACGGCAGAGATGTCCTGAGACACCCCAGCCTGGCCGCAGAAGAGCGTATGG
                                                                                                                                                                                                                    HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
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                                                                                                                                                                                                                                                                                                       GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5256554"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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BI904605
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421

140 481 541

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242

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A1326391 782 bp mRNA linear EST 23-DEC-1998 mm18f09.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:521897 3' similar to gb:U03714 Mus musculus BALB/c alpha 1 type XVIII collagen (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                       This clone was previously sequenced on the 5' end only, this new data is from the 3' end High quality sequence stop: 453.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:315745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HisThrHisGlnAspPheGlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
Washb-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/organism="Mus musculus"
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/clone="IMAGE:521897"
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Fax: 314 286 1810
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/dev stage="s months"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM11053 row: j column: 01
High quality sequence stop: 796.
Location/Cualifiers
Location/Cualifiers
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/mol_type="mRNA"
/strażn="FVB/N-3"
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/done lib="MIA Mouse 15K CDNA Clone Set"
//done lib="MIA Mouse 15K CDNA Clone Set"
//note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; This clone is among a rearrayed Set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of ET:5 embryos.
// and El2.5 female mesonephros/gonad) and one newborn ovary CDNA library. Average insert size 1:5 kb. All source libraries are cloned unidirectionally with Oligo (dT )-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U SA, 97: 9127-9132; (2) Large-scale CDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcribte from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 167-1978."
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|ibraries"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 LeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ArgArgAlaAspArgThrGlyValProValValAsnLeuArgAspGluValLeuPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 SerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLysProGlyAlaArgilePhe
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
Mational Institute on Aging/National Aging
Email: cdnaelgsun.grc.nia.nih.gov
This clone aget has been freely distributed to the community. Please
Plate: H3111 row: D column: 11
Seq primer: -21M13 Forward
High quality sequence stop: 733
POUNA=Yes.
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H3111D11-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3111D11 3', mRNA sequence.
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1 (bases 1 to 733)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H.

111, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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                   GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
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BUBS9398 944 bp mRNA linear EST 16-OCT-2002 AGENCOURT 10434549 NIH MGC 109 Homo sapiens cDNA clone IMAGE:6650260 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loases L to 344,

NIH-WGC http://mgc.nni.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Precurement: ArCc

CDNA Library Preparation: Rubin Laboratory

CONA Library Preparation: Rubin Laboratory

CONA Library Preparation: Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.lln.gov

Plate: LLCM2895 row: d column: 04

High quality sequence stop: 572.
                                                                                                                                    GlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThrGluAlaProAlaAlaThr 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 944)
                                                                                                                                                                                                                             147 GlyGlnAlaSerSerLeuLeuAlaGlyArgLeuLeuGluGlnGluAlaAlaSerCysArg
PheSerGlySerGluGlyGlnLeuLysProGlyAlaArgllePheSerPheAspGlyArg
                   241 TTTCTGGCTCCCAGGGTCAACTGCAACCCGGGGCCCGCATCTTTTCTTTTGACGGCAGA
                                                                    107 AspValLeuGlnHisProAlaTrpProArgLysSerValTrpHisGlySerAspProSer
                                                                                       Length:
Matches:
Conservative:
Mismatches:

    . 944
    /organism="Homo sapiens"

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784.00
92.44%
83.72%
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Homo sapiens
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Best Local Similarity:
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602960041P1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5125523 5',
mRNA sequence.
BI247582
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 723)
11 (bases ttp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnLeuValLeuHisLeuValAlaLeuAsnSerProGlnProGlyGlyMetArgGlyIle 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:5125523"
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Site_2: Sall; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 1:9 kb. Constructed by Life
Technologies. Note: this is a NCT_CGAP_Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCCAGTGCTCCACTGGTGGCACTGAACACCCCCCTGTCTGGAGGGATGCGTGGTATC
                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1307 row: a column: 12
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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81 GGAGGCATGCGTGGTATCCGTGGAGCAGATTTCCAGTGCTTCCAGCAAGCCCGAGCCGTG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 GluAlaAlaSerCysArgHisAlaPheValValLeuCysIleGluAsnSerValMetThr 180
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/tissue_Iype="spontaneous tumor, metastatic to mammary.
Stem cell origin."
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/clone_lib="WIXI CGAP_Lu29"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 272 c 264 g 195 t
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Mismatches:
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Job time : 1633.67 secs
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601776586F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4018317 5',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                         110 GlnHisProAlaTrpProArgLysSerValTrpHisGlySerAspProSerGlyArgArg 129
                                                                                                                                                                                                                                                                                                                                                                                                                         LeuThrAspSerTyrCysGluThrTrpArgThrGluAlaProAlaAlaThrGlyGlnAla 149
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.
                                                                             LeuHisLeuValAlaLeuAsnSerProGlnProGlyGlyMetArgGlyIleArgGlyAla
                                                                                                                                                                           CTGACCGAGAGCTACTGTGAGACGTGGCGGACGGAGGCTCCCTCGGCCACGGGCCAGGCC
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                                                                                                                                             AspPheGlnCysPheGlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAlaPhe
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High quality sequence stop: 722.
Location/Qualifiers
Indels:
Gaps:
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                             x BU859398 (1-944)
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/strain="CZECH II"
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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Methods and compositions for diagnosing and involving angiogeneeis
Patent: EP 1191036-A 1 27-MAR-2002;
Pfizer Products Inc. (US)
Location/Qualifiers
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Sequence 3 from Patent EP1191036.
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Sheppard, M.G. and Tong, X.
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FPGRDILLGOSAWPQKSIWHGSDAKRRLPESYCEAWRTDERGTSGQASSLSSGKLLEG
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AITDSTQSIIYVGVKLSDLQMGKQQIIFYYTEPGSQSSYAAATFTVPTLLNQWTRFAI
SVEEDEVILYLDCEEHERVRFERSPDEMELEEGSGLFVAQAGGADPDKYQGVIADLRL
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SASLRGDKGEAGPKGEKGEPGSSTLYGPSVTGPPGPQGYPGPPGPKGDSIVGPPGPPG
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1 (bases 1 to 5279)
Halfter, W., Dong, S., Schurer, B. and Cole, G.J.

Collagen XVIII is a basement membrane heparan sulfate proteoglycan J. Biol. Chem. 273 (39), 25404-25412 (1998)
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Halfer,W. and Dong,S.
Direct Submission
Submitted (11-AUG-1998) Neurobiology, University of Pittsburgh, 3500 Terrace Street, Pittsburgh, PA 15261, USA
Halfter,W. and Dong,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (31-AUG-2001) Neurobiology, University of Pittsburgh, 3500 Terrace Street, Pittsburgh, PA 15261, USA Sequence update by submitter
On Aug 31, 2001 this sequence version replaced gi:3493142.
Location/Qualifiers
                                                                                    AF083440 5279 bp mRNA linear Gallus gallus sollagen XVIII mRNA, complete cds. AF083440
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/mol_type="mRNA"
/db_xref="taxon:9031"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 534)
O'Reilly,M.S. and Folkman,M.Judah.
Therapeutic antiangiogenic endostatin compositions
Patent: US 6346510-A 6 12-FEB-2002;
Location/Qualifiers
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AX100092
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Sequence 6 from patent US 6346510.
AR193166 GI:20239131
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PAT 18-MAY-2002
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Angiostatin and endostatin binding proteins and methods of
Patent: Wo 0193897-A 30 13-DEC-2001;
EntreMed, Inc. (US)
                                 Liang, H., Sim, K.L., Chang-Murad, A., Zhou, X., Madsen, J.,
Boerner, R.J., Bermejo, L.L., Mistry, F.R., Shepard, S.R. and
Schrimsher, J.L.
Method of producing and purifying endostatin?tm protein
Patent: WO 0119989-A 4 22-MAR-2001;
EntreMed, Inc. (US)
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196 c 179 g 94
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AX395662
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Neallly,M.S. and Folkman,M.Judah.
Therapeutic antiangiogenic endostatin compositions
Patent: US 6346510-A 4 12-FEB-2002;
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Sequence 4 from patent US 6346510.
AR193165
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Sequence 4 from Patent WO0119989.
AX100086 GI:13539061
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RESULT 9 AX473835

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             CO7KI4/56,
CO7KI4/78,C12N9/68,C12N15/00,A61K37/02
Pused protein containing angiostatin component and utilization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z (bases I to 555)
Zhi-Yong, H., Biao, L., Wei-Jie, Z. and Xiang-Fu, W.
Direct Submission
Submitted (07-SEP-1999) Shanghai Institute of Biochemistry, Chinese Academy of Sciences, 320 Yueyang Road, Shanghai 200031, P. R. China Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRI 06-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 558) Exil-Yong, H., Biao, L., Wei-Jie, Z. and Xiang-Fu, W. Cloning and expression of human endostatin gene in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C12N15/09, A61K38/00, A61K48/00, A61P9/10, A61P35/00, C07K14/52,
                                                                                                  AF184060 Spiens type XVIII collagen mRNA, complete cds. AF184060.1 GI:6013264
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 52)

S Bolanowski, M.A., Caparon, M.H., Casperson, G.F., Gregory, S.A.,

Klein, B.K. and Mckearn, J.P.

Pused protein contening angiostatin component and utilization

thereof in antitumor therapy

LD Patent JP 2001518304-A 50 16-OCT-2001;

GD SEARLE AND CO

S Homo sapiens (human)

PN 2001518304-A/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 bp DNA linear PAT 27-AUG-2002
Fused protein containing anglostatin component and utilization
EDD081407
                                                                                                PAT 09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGGCTGGCGGCCCTTCCGCCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180
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30-5EP-1997 US 60/060609
MARK A BOLANOWSKI, MAIRE H CAPARON, GERALD F CASPERSON, SUSAN A GREGORY,
BARBARA K KLEIN, JOHN P MCKEARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                                                                       Sim, K.L. and Liang, H.
Angiogenesis-ignibiting peptides and proteins and methods of
Patent: WO 0210982-A 2 18-APR-2002;
EntreMed, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Sequence 2 from Patent WO0230982
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JP 2001518304-A/50.
Homo sapiens (human)
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Score: Pred.

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Homo sapiens multi-functional protein MFP mRNA, complete cds.
AF282883
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 786)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 650
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                                                                                                               41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
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                                                                                                                                                                                                                                                                        linear
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Sequence 14 from Patent WO0210372.
                                                                               US-09-938-391-4 (1-184) x AF416592 (1-564)
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AF282883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to endostatin; can inhibit endothelial cell
proliferation"
                                                                                                                                                                                                                                                                                                                                                      PRI 02-DEC-2001
                                                                                                                                                                                                          3 (bases 1 to 564)
Feng,Y., Cui,L.B. and Ma,Q.J.
Direct Submission
Submitted Sisse-2001) Genetic Engineering, Beijing Institute of
Biotechnology, Taiping Road, Beijing 100850, P.R. China
Location/Qualifiers
                                                                                                                                                                                             9
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                                                                                                                                                                                        GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 564)
Feng, Y., Wu, Y., Zhu, X., Liu, C.X. and Ma, Q.J.
Endostatin contributes to maintain cartilage homeostasis via promotion of the anabolic program of chondrocytes unpublished
                                                                                                                                                                                                                                                                                                                                            Araloby2
Homo sapiens collagen XVIII mRNA, partial cds.
AF416592
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Sheng Wu Gong Cheng Xue Bao 17 (3), 278-282 (2001)
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                                                                                                                              Gaps:
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239 C 280 G 143 L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Mile Road, Suite 24-26, Redford, MI 48239, USA
Location/Qualifiers
1. 786
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41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerlle 60

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Canine pro-endosta Canine angiogenesi Chicken endostatin Alternate human en Human gene fragmen

Canine endostatin

Description

and is derived by analysis of the total score distribution

Human gene fragmen Human endostatin c Human angiogenesis Human angiogenesis

Human endostatin Human endostatin

SEQ ID 50 of WO991 Nucleotide sequenc

Human endostatin endostatin

Human endostatin

Human endostatin c Human vasculār end Human endostatin c

Human

cDNA encoding huma

Human pancreatic c Human endostatin e

Human endostatin

Specific tumour ce

Run on:

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Dog; pro-endostatin; endostatin, angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; heemophiliac joints; angiofibroma; wound granulation; coronary collateral; cerebral collateral; arteriovenous malformation;
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- 2003 Compugen Ltd.
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    nucleic search, using frame_plus_p2n model

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Reproductive recom Anticancer gene-as Synthetic plasmid DNA encoding a hum Synthetic plasmid Nucleotide sequenc DNA encoding human Human alpha-1 coll Human alpha-1 coll

Gene #2178 used to

Human pancreatic

collagen XV1 Human ovarian anti

Human

Nucleotide sequenc Human immune/haema

Human collagen 18

Human immune/haema

Murine angiogenesi Murine endostatin

Mouse endostatin

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Dog; pro-endostatin; endostatin; angiogenesis; cancer; gene therapy; psoriasis; rheumatoid arthritis; retinopathy; macular degeneration; corneal graft rejection, neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joints; angiofibroma; wound granulation; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; diabetic neovascularisation; fracture; cerebral collateral; arteriovenous malformation; optimation; antipsoriatic; antidiabetic; ophthalmological;
                                      ProSerTrpGluAlaLeuPheSerGlySerGluGlyGlnLeuLy8ProGlyAlaArgIle 100
                                                                                                           PheSerPheAspGlyArgAspValLeuGlnHisProAlaTrpProArgLysSerValTrp 120
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                                                           241 CCCAGCTGGGAGGCCTTATTCTCGGCTCCCAAGGCCCAGCTGAAGCCCGGGGCCCCCGCATC
                                                                                                                                                                                    HisGlySerAspProSerGlyArgArgLeuThrAspSerTyrCysGluThrTrpArgThr
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/*tag= a
/product= "pro-endostatin"
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iscnaemic limb angiogenesis; diabetic neovascularisation; fracture;
cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological;
gynaecological; gene; ss.
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                                                                                                                                  Location/Qualifiers
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                                  Canine; immunoglobulin Fc fragment; endostatin; immunofusin;
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                Canine angiogenesis inhibitor, endostatin DNA.
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Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -

Example 8; Pages 58-59; 68pp; English.

inte parenta utastoases a nowa misserie encotating a rustion procession a signal sequence, an immunoglobulin For region, and an anglogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including conditions the meangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, remumeroid arthritis, psoriasis, coular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental citizoplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a DNA encotaining canine construction of immunofusin containing canine The patent discloses a DNA molecule encoding a fusion protein comprising immunoqlobulin Fc fragment

Sequence 552 BP; 77 A; 204 C; 190 G; 81 T; 0 other;

Alignment Scores:			
Pred. No.:	6.82e-159	Length:	55
Score:	176.00	Matches:	17
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	95.65%	Indels:	0
DB:	21	Gaps:	0

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AAZ51309

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Disclosure; Page 115-116; 146pp; English.
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                                                                                                                                                               145 TTCCTGTCGTCGCGGCTGCAGGACCTCTACAGCATCGTGCGCCGCGCCGACCGCACCGCG
                                                                            GTGCTGCACCTGGTGGCCCTGAACAGCCCGCAGCCGGGCGGCATCCGAGGCATCCGGGGA
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                                                                                                                                     AlaAspPheGlnCysPheGlnGlnAlaArgAlaAlaGlyLeuAlaGlyThrPheArgAla
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                                                     ValLeuHisLeuValAlaLeuAsnSerProGlnProGlyGlyMetArgGlyIleArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endostatin, antiangiogenic, angiogenesis, human, mouse, chicken, cancer, inflammation, angiogenesis-dependent disease, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken endostatin coding sequence SEQ ID NO: 5.
              US-09-938-391-4 (1-184) x AAZ51309 (1-552)
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The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancers, inflammation, rheumatoid arthritis, chronic articular rheumatism, psoriasis, disorders associated with inopportune invasion of vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy of prematurity, macular degeneration, corneal graft rejection, retrolantal fibroplasia, rubeosis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent diseases include Osler Webber syndrome, myocardial angiogenesis, plaque neovasculisation, telangiectesia, haemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerI]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angiogenesis; telangiectasia; angiofibroma;
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Matches:
Conservative:
Mismatches:
Indels:
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/product= "Endostatin protein"
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99US-0315689.
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Homo sapiens.

The present sequence encodes an alternate functional endostatin

protein. When the human endostatin gene sequence AAA27004 is

recombinantly expressed, an observable doublet of protein results, both

versions of which are functional endostatin proteins. The present gene

sequence encodes an endostatin variant which is the same as the protein

ceded by AAA27004 minus the first four amino acids. Recombinant mouse

encoded by AAA27004 minus the first four amino acids. Recombinant mouse

conditions and administered subcutaneously to mice implanted

with Lewis lung carcinomas. There was tumour mass regression

con-detectable levels after 12 days of therapy due to the angiogenesis

inhibitory activity of endostatin. Thus the protein is useful for

treatment of angiogenesis- dependent cancers. The polymucleotide and

colypeptide sequences of this endostatin are useful for treating and

colypeptide sequences of this endostatin are useful for treating and

colypeptide sequences, plaque neovascularisation, telangiectasia,

myocardial angiogenesis, plaque neovascularisation, telangiectasia,

calls e.g. intestinal adhesions, atherosclerosis, scleroderma. The

protein may also be useful as a birth control agent by reducing or

protein may also be useful as a birth control agent by reducing or

preventing uterine vascularisation. The gene for endostatin may be

continue cells of indostatin may be

continue cells of endostatin may necessary and the express high levels of endostatin, eg. tumour cells, by generating cDNA from mRNA using reverse transcriptase and then amplifying the DNA sequence. Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers and as birth control agents Claim 11; Page 40; 68pp; English 2000-365617/31. P-PSDB; AAY94324 

Sequence 534 BP; 77 A; 189 C; 175 G; 93 T; 0 other;

534 00 00 00 00 Matches: Conservative: Mismatches: Indels: Length: 1.55e-15 26.00 100.00% 100.00% 14.13% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

US-09-938-391-4 (1-184) x AAA27005 (1-534)

109 degetréecegecAcerrécecécerrécrerecréececrecadeacereracadecare 168 41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerlle 60 169 Grececereceaces 186 99 ValArgArgAlaAspArg 61 g Š 셤

AAS00868 standard; DNA; 537

RESULT 6

ВЪ.

AAS00868;

(first entry) 04-JUL-2001

Human, Endostatin(TM); angiogenesis mediated disease, solid tumours; blood borne tumour; leukaemia, tumour metastasis, benign tumour, haemangioma, acoustic neuroma; neurofibroma; trachoma; rubeosis; pyogenic granuloma; rheumatoid arthritis; psoriasis; colon cancer; ocular angiogenic disease, diabetic retinopathy; macular degeneration; retinopathy of prematurity; macular corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; Osler Webber Syndrome; Human gene fragment encoding Endostatin(TM) N-terminal mutant protein. myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; mutant; ds. 

/note= "Variant produced during fermentation reaction of Pichia pastoris harbouring an expression plasmid containing the present sequence" 'note= "Neither of the above CDSs have start or stop /\*tag= a /product= "Endostatin(TM) N-terminal mutant#1" /\*tag= b /product= "Endostatin(TM) N-terminal mutant#2" ocation/Qualifiers 'partial codons" ..540 

WO200119989-A2

22-MAR-2001.

14-SEP-2000; 2000WO-US25166.

14-SEP-1999;

(ENTR-) ENTREMED INC.

Boerner RJ; Liang H, Sim KL, Chang-Murad A, Zhou X, Madsen J, Bermejo LL, Mistry FR, Shepard SR, Schrimsher JL;

2001-244802/25

P-PSDB; AAU00901, AAU00900.

Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumours, comprises recombinantly producing the protein using an expression system, and recovering and purifying the protein

Claim 6; Page 32; 67pp; English.

The sequence encodes Human Endostatin(TW) N-terminal deletion

mutant lacking the N-terminal 4 amino acids. The new method of the

mutant lacking the N-terminal 4 amino acids. The new method of the

invention is useful for producing, recovering and purifying Endostatin

(TW) from biological sources, such as biological fluids, tissues, cells,

culture media, and fermentation media. Endostatin(TM) is useful for

treating angiogenesis mediated diseases such as solid tumours, blood

control tumours, leukaemias, tumour metastases, benign tumours, e.g.

the managioma, acoustic neurcomas, neurofibromas, trachomas, and pyogenic

control tracing arthritis, psoriasis, ocular angiogenic diseases,

control tracing arthritis, psoriasis, ocular angiogenic diseases,

concer, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome,

concer, retrolental fibroplasia, rubeosis,

concer, retrolental fibroplasia,

Sequence 537 BP; 79 A; 189 C; 176 G; 93 T; 0 other;

537 26 0 0 Conservative: Mismatches: Indels: Matches: Length: 1.56e-15 26.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: Pred. No.:

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                                                             GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers and as birth control agents
                                                                                                                                                                                                                                                                     Human; endothelial cell proliferation inhibitor; collagen XVIII; angiogenesis inhibitor; anti-tumour; cytostatic; antipsoriatic; vasotropic; determatological; ophthalmological; vulnerary; antiarteriosclerotic; antidiabetic; haemostatic; contraceptive; coular angiogenic disease; atherosclerosis; scleroderma;
                                                                                                                                                                                                                                                                                                                                    angiogenesis; telangiectasia; angiofibroma;
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Endostatin protein"
 Gaps:
                        US-09-938-391-4 (1-184) x AAS00868 (1-537)
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                                                                                                 ValArgArgAlaAspArg
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                                                                                                                                                                        AAA27004 standard; DNA; 546
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/product=
                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                              Human endostatin gene.
22
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20-MAY-1999;
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wound granu
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vascularisation. The gene for endostatin may be isolated from cells or tissue that express high levels of endostatin, eg. tumour cells, by generating cDNA from mRNA using reverse transcriptase and then amplifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasminogen; human; angiostatin; endostatin; gene therapy; vector; anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                                                                Sequence 546 BP; 80 A; 196 C; 177 G; 93 T; 0 other;
                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 Grececereceseces 198
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                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                the DNA sequence.
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Gaps:

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121 GGCTGCCGGCCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180
                                                                                                                                                                                                                                                                       Human; immunoglobulin gamma Fc fragment; endostatin; immunofusin; angiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; collar angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularisation; telanglectasia; wound granulation; keloid scar; gene therapy; ss.
                                       41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Does not include stop codon"
                                                                                                                                                                                                                                                Human angiogenesis inhibitor, endostatin cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product= "Endostatin"
             US-09-938-391-4 (1-184) x AAA29884 (1-549)
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                     AAZ51291 standard; cDNA; 549
                                                                                      61 ValArgArgAlaAspArg
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P-PSDB; AAY70252.
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                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
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                                                                                                                                                                                              121 GGGCTGGCGGGCACCTTCCGCGCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes an angiogenesis inhibiting factor (1), designated IAF-1. The present invention also describes: (1) preparation of (1) and its derivative; (2) an IAF binding acceptor and its preparation; and (3) an IAF antibody. (1) is useful for preparing new bological preparations for effectively treating various tumours and abnormal-vessel diseases. The IAF antibody is preferably a polyclonal antibody, mosaic antibody, single stranded antibody and human originated
                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Angiogenesis inhibiting factor 1 and its derivative useful for treating
                                                                                                                                                       41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                                                                                                                                                                                                    Human; anglogenesis inhibiting factor 1; IAF-1; tumour; antibody; abnormal vessel disease; ss.
                                                                                                                                                                                                                                                                                                                                                                 Human angiogenesis inhibiting factor 1 encoding cDNA.
                                     BP; 82 A; 196 C; 178 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
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                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                            US-09-938-391-4 (1-184) x AAX77719 (1-549)
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                                                                                                                                                                                                                                                                                     AAA29884 standard; cDNA; 549 BP.
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                                    1.59e-15
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P-PSDB; AAY90771.
                                                            Percent Similarity:
Best Local Similarity:
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Sequence 549
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                        Alignment Scores:
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DB:
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a signal sequence, an immunoglobulin Fc region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses a DNA molecule encoding a fusion protein comprising
                                                                                                                                                                                                                                                                                                Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Pages 40-41; 68pp; English
Lo K, Li Y, Gillies SD;
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549 26 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

1.59e-15 26.00 100.00% 100.00% 14.13%

Score: Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

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fibroplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints' angiofibroma, wound granulation, and excessive or abnormal stimulation of endochelial cells, intestinal cells, atherosclerosis, sclerodermal and hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a cDNA encoding human endostatin used in the construction of immunofusin containing human immunoglobulin gamma (IgG) Fc fragment.

Note: This sequence is stated in claim 12 as being amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            refers to this sequence as being nucleotide sequence of human endostatin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Endostatin(TM); angiogenesis mediated disease; solid tumours; blood borne tumour; lgukaemia; tumour metastasis; benign tumour; haemangioma; acoustic heuroma; neurofibroma; trachoma; rubeomis; pyogenic granuloma; rheumatoid arthritis; psoriasis; colon cancer; ocular angiogenic disease; diabetic retinopathy; macular degeneration; retinopathy of prematurity; macular corneal graft rejection; neovascular glauçoma; retrolental fibroplasia; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasis; plaque neovascularisation; telangiectasis; haemophiliac joint; angiofibroma; wound granulation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                             41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes "Variant produced during fermentation reaction of Pichia pastoris harbouring an expression plasmid containing the present sequence"
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                                                                                                                                                             plasminogen fragment, however, the rest of the specification
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product= "Endostatin(TM) C-terminus minus 3"
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product= "Endostatin(TM) C-terminus minus 1"
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                                                                                                                                                                                                              Sequence 549 BP; 82 A; 196 C; 178 G; 93 T; 0 other;
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Matches:
Conservative:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                         Query Match:
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AAS00867
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ince sequence accourate numera survolentariary, inte new merchou of Life invention is useful for producing, recovering and purifying Endostatin (TM) from biological sources, such as biological fluids, tissues, cells, culture media, and fermentation media. Endostatin (TM) is useful for treating andiogenesis mediated diseases such as solid tumcurs, blood borne tumcurs, leukaemias, tumcur metastases, benign tumcurs, e.g. treathomas, acoustic neuromas, neurofibromas, trachomas, e.g. granulomas, rheumatcid arthritis, psoriasis, ocular angiogenic diseases, c.g., diabetic retinopathy, retinopathy of prematurity, macular c.g. degeneration, corneal graft redjection, neovascular glaucoma, colon cancer, retrolental fibroplasia, rubbosis, Osler-Webber Syndrome, c.g. myocardial angiogenesis, plaque neovascularisation, telangiectasia, myocardial angiogenesis, plaque neovascularisation, telangiectasia, concer, retrolental fibroplasia, rubbosis, Osler-Webber Syndrome, c.g. neemphilias joints, angiofibroma, and wound granulation. Endostatin(TM) is also useful for treating disease of excessive or abnormal stimulation of endothelial cells such as intestinal adhesions, atherosclerosis, c.g. endostatin(TM) can be stored in buffers for extended periods of time, and biologically active Endostatin(TM) are obtained by the new method.

C. Endostatin(TM) can be stored in buffers for extended periods of time, and also subjected to lyophilisation, while preserving biological activity: Centrifugation of broth from fermentation steps in production is avoided, or additional proteins, pigments, enzymes and other cellular chemicals and additional proteins, pigments, enzymes and other cellular chemicals and
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                                                                                                                                      /note= "None of the above CDSs have start or stop codons"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing Endostatin protein for treating angiogenesis mediated diseases such as solid tumours, comprises recombinantly producing the protein using an expression system, and recovering and purifying the
                reaction of Pichia pastoris harbouring an expression plasmid containing the present sequence"
                                                                                                                                                                                                                                                                                                                                                                              Boerner RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence encodes Human Endostatin(TM). The new method of the
produced during fermentation
                                                                                                                                                                                                                                                                                                                                                                            Zhou X, Madsen J,
, Schrimsher JL;
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Mismatches:
Indels:
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Matches:
                                                                                                 'product= "Endostatin(TM)"
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                                                                                                                                                                                                                                                                                                                                                                              Chang-Murad A, Zh
y FR, Shepard SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 29; 67pp; English.
'note= "Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValArgArgAlaAspArg 66
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Bermejo LL, Mistry FR,
                                                                                                                      partial,
                                                       ..549
                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                         (ENTR-) ENTREMED INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-244802/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                     22-MAR-2001
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DB:
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Endostatin, human, ophthalmological; ocular neovascularisation; choroidal neovascularisation; gene therapy; gene; ss.

Human endostatin coding sequence.

(first entry)

05-DEC-2002

ABQ81193;

ABO81193 standard; cDNA; 551 BP

RESULT 13 ABQ81193

99

61 ValArgArgAlaAspArg

181 Grececereceaces

Location/Qualifiers

Homo sapiens

ø partial 1..551 /\*tag=

product= "Endostatin"
/transl\_except= "(pos:2..3,aa:His)"
/note= "the CDS does not include a start codon"

Dixon KH;

Brazzell RK, Campochiaro PA,

WPI; 2002-698636/75.

(NOVS ) NOVARTIS AG.

22-FEB-2001; 2001US-270787P. 04-APR-2001; 2001US-281296P.

21-FEB-2002; 2002WO-US05336.

WO200267971-A2

06-SEP-2002

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This sequence encodes endostatin. Endostatin is a 20 kD C-terminal fragment of collagen XVIII that inhibits angiogenesis. The endostatin coding sequence may be used in the recombinant viral vector of the invention for obtaining angiostatin activity. The vector comprises a promoter capable of expressing human angiostatin operably linked to a protect capable of expressing human angiostatin operably linked to a fartuctural gene encoding one or more domains of human angiostatin. The vector, which may be a replication-defective viral vector, is useful for inhibiting angiogenesis in a mammal, especially with cancer or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant viral vector expressing human angiostatin useful for inhibiting angiogenesis in a mammalian subject with cancer or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: This sequence is given incorrectly in the sequence listing of
the specification as an amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mendez M;
                                                                                                                                                                                                       Gene; human; plasminogen; angiostatin; neovascularisation;
kringle domain; cell proliferation; viral vector;
replication-defective; cancer; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 549 BP; 82 A3 196 C; 178 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patel S, Jooss K,
                                                                                                                                                                                                                                                                                                                                                     /product= "Endostatin"
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                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                           Human endostatin coding sequence. .
GTGCGCCGTGCCGACCGC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chang B, Wu WW, Macarthur J,
                                                                            ABA00774 standard; cDNA; 549
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                                                                                                                                           (first entry)
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P-PSDB; AAG79753.
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                                                                                                             ABA00774;
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                                              RESULT 12
                                                                ABA0077
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The present sequence is a partial coding sequence for human endostatin. A claimed method for the treatment of ocular endostatin. A claimed method for the treatment of ocular encovacularisation, especially choroidal neovascularisation, involves increasing the level of endostatin in ocular tissue, especially where the endostatin is encoded by the present sequence, or is its fragment, derivative or variant. The increase is effected by administering a retrovirus or lentivirus vector, adeno-associated virus, a retrovirus or lentivirus vector, comprising an endostatin-encoding nucleic acid. Cells secreting endostatin may be encapsulated and implanted within an individual. The method is used when ocular neovascularisation is caused by istoplasmosis, pathological myopia, angioid streaks, anterior ischaemic optic neuropathy, bacterial endocarditis, Best's disease, birdshot retinochoroidopathy, choroidal osteomas, choroidal cupture, choroidal nonperfusion, choroidal osteomas, choroidal cupture, choroidelenaemia, chronic retinal detachment, coloboma of the retina, brusen, endoseous Candida endophthalmitis, extrapapillary hamartoma of the retinal pigmented epithelium, extrapapillary hamartoma of the retinal pigmented epithelium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating or preventing choroidal neovascularization comprises increasing the amount of endostatin in ocular tissues of afflicted individuals to a choroidal neovascularization inhibiting level -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fundus flavimaculatus, idiopathic, macular hole, malignant melanoma, membranproliferative glomerulonephritis (type II), metallic intraocular foreign body, morning glory disc syndrome, mutiple evanescent white-odc syndrome, neovascularisation of ora serrata, operating microscope burn, optic nerve head pits, photocoagulation, punctate inner choroidopathy, rubella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Page 39-40; 44pp; English.
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121 GGGCTGGGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180

41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 60

00000 00000 0

Conservative: Mismatches: Indels:

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores: Pred. No.:

Gaps:

US-09-938-391-4 (1-184) x ABA00774 (1-549)

Length: Matches:

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anti-angiogenic and/or anti-tumor activity. The multifunctional protein
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                                                                                                                                                                                                                                                                                           120 GGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 179
                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                      41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have
fluid drainage, tiled disc syndrome, Toxoplasma retinochoroiditis, tuberculosis, Vog-Koyanagi-Harada syndrome, diabetic retinopathy, non-diabetic retinopathy, arin vein occlusion, central retinopathy, vein occlusion, retinopathy in premature infants, rubeosis iridis, neovascular glaucoma, perifoveal telangiectasis, sickle cell retinopathy, Eale's disease, retinal vasculitis, Von Hippel Lindau disease, radiation retinopathy, retinal cryoinjury, retinitis pigmentosa, retinochoroidal coloboma, corneal neovascularisation due to herpes simplex keratitis, corneal ulcers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiostatin; endostatin; interferon; thrombosponain; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis;
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                                                                                                                                    Sequence 551 BP; 83 A; 195 C; 179 G; 94 T; 0 other;
                                                                                                                keratoplasty, pterigyia and trauma (all claimed).
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Matches:
Conservative:
Mismatches:
Indels:
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Klein BK, McKearn JP;
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Best Local Similarity:
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Pred. No.:
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may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of human endostatin encoded by plasmid pMALCH#15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces sp. strain C5; SnpA; S. venezuelae; alpha-amylase; endostatin; cancer; tumour growth; angiogenesis; ss.
                                                                                                                                                                                                                                                                                                                                                               252
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                                                                                                                                                                                                                                                                                   Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;
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Matches:
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The present sequence encodes human endostatin. The protein is expressed in Streptomyces. Leader sequences of Streptomyces sp. strain C5 anp and S. venezuelae alpha-amylase proteins are linked to the S. venezuelae alpha-amylase proteins are linked to the N-terminal of endostatin. This ensures that endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. The method is used for preparing soluble recombinant human, murine or primate endostatin, which is useful in the treatment of cancer. Inhibition of tumour growth, inhibition of angiogeneiss, isolation of receptors for endostatin and for identification of anti-angiogenic compounds in assays. The endostatin protein is produced as a secreted, soluble protein which needs no refolding, is stable in the fermentation broth and is produced in large quantities. Streptomycetes are amenable for cultivation in large fermentations allowing for large quantities of soluble endostatin to be produced. 

Sequence 552 BP; 83 A; 196 C; 179 G; 94 T; 0 other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1.6e-15 26.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match:

US-09-938-391-4 (1-184) x AAC62023 (1-552)

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: O'REALILY, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
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US-09-107-532A-1972

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US-09-313-581-1

US-09-315-81-1

US-09-315-81-14

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US-08-96-95-98
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Conservative:
Mismatches:
Indels:
 US-09-620-312D-1012
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US-08-437-667-97
US-08-906-955-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09315689
Patent No. 6346510
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1823 - 508 800 1001 1001 1305 4748 5798 7286 7286 29604 29604 111282
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
  Alignment Scores:
Pred. No.:
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US-09-315-689-6
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   SEQ ID NO 6
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-MODEL=frame+ p2n.model -DEV=xlp
-O=/Cogn2 1/USPETO spool p./USO9938391/runat 04082003_130739_27621/app_query.fasta_1.718
-O=/Cogn2_1/USPETO spool_p./USO9938391/runat 04082003_130739_27621/app_query.fasta_1.718
-USOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=Oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-USTRT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=USO9938391_@CGN_1 1 133 @runat 04082003_130739_27621 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-USER=USO9938391_@CGN_1 1 133 @runat 04082003_130739_27621 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-USER=TANGEOUP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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30, Appl
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3, Appli
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37, Appli
                                                                           August 18, 2003, 00:40:31; Search time 57.3333 Seconds (without alignments) 1416.532 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 12,
Sequence 1,
                                                                                                                                    184
1 HTHQDFQLVLHLVALNSPQP......CRHAFVVLCIENSVMTSFSK 184
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
            GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                       nucleic search, using frame_plus_p2n model
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US-09-315-689-4
US-09-20-05-30
US-08-159-784-4
US-09-449-293-3
US-09-75-325-3
US-09-965-526-37
US-09-561-108-12
US-09-561-108-12
US-09-561-526-12
US-09-561-499-12
US-09-561-499-12
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Maximum DB seq length: 200000000
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Result 8

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181 GTGCGCGTGCCGACCGC 198
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Best Local Similarity:
Query Match:
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US-08-159-784-4
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                                                                            US-08-159-784-4
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PREENT NO. 6201104
GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas
APPLICANT: Sim, Kim Lee
TITLE OF INVENTION: Anglogenesis-Inhibiting Protein Binding Peptides and
TITLE OF INVENTION: Proteins and Methods of Use
TITLE OF INVENTION: Proteins and Methods of Use
TITLE REFERENCE: 05513-0370
CURRENT APPLICATION NUMBER: US/09/206,059
CURRENT PILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 30
                                                                                                        APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0233-029
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 546
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Matches:
Conservative:
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Matches:
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                                                       Sequence 4, Application US/09315689
Patent No. 6346510
GENERAL INFORMATION:
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, ORGANISM: Homo sapiens
US-09-315-689-4
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Query Match:
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US-09-206-059-30
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LENGTH: 552
                                       US-09-315-689-4
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1624 GGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 1683
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Sequence 4, Application US/08159784
Patent No. 5643783
GENERAL INFORTION:
GENERAL INFORTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZURP 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: TBM PS/2 Model 56Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/159,784
FILLING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-449-293-3
; Sequence 3, Application US/09449293
; Patent No. 6267954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.02e-16
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APPLICANT: Abitbol, Marc
APPLICANT: Uteza, Yves
APPLICANT: Menasche, Maurice
APPLICANT: Bossard, Carine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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63

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133 GGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATCGTGCGCCGT 192
 44 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArg
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
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Matches:
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APPLICATION WUMBER:
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCMORTON INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                                                                                     ; Sequence 37, Application US/08985526
; Patent No. 6080728
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Sequence 12, Application US/09561500
Patent No. 6342219
GENERAL INFORMATION:
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TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                          64 AlaAspArg 66
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STATE: Delaware
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Delaware
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Best Local Similarity:
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CLASSIFICATION:
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                             APPLICANT: Prats, Herve
APPLICANT: Prats, Herve
APPLICANT: Honiger, Jiri
APPLICANT: Honiger, Jiri
APPLICANT: Honiger, Jiri
APPLICANT: Numer-Jahle? Martin
TITLE OF INVENTION: INTRACOULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076_202US01
CURRENT APPLICATION NUMBER: US/09/449,293
CURRENT APPLICATION NUMBER: 1999-11-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENTH: 558
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APPLICANT: Honiger, Jiri
APPLICANT: Neuner-Jehle, Martin
TITLE OF INVENTION: INTRAOCULAR TRANSPLANTATION OF ENCAPSULATED CELLS
FILE REFERENCE: 8076.20201801
CURRENT APPLICATION NUMBER: US/09/775,325
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: US 99/449,293
PRIOR FILING DATE: 1999-11-24
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Matches:
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Mismatches:
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Mismatches:
Indels:
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Menasche, Maurice
Bossard, Carine
Van Den Berghe, Loic
Bonnel, Sebastian
Prats, Herve
APPLICANT: Van Den Berghe, Loic APPLICANT: Bonnel, Sebastien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                              ) ORGANISM: Rattus rattus US-09-449-293-3
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Best Local Similarity:
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Best Local Similarity:
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LENGTH: 558
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US-09-775-325-3
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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GENERAL INFORMATION:

APPLICANT: Mixson, James A

TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA

TITLE OF INVENTION: ENCODING ANTI-ANGIGGENIC PEPTIDES AND THEIR USE IN GENE

TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Connolly, Bove, Lodge, & Hutz

STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 GGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATCGTGCGCCGT 199
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Sequence 12, Application US/09561526
Fatent No. 6416758
Fatent No. 6416758
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION:
FILE REFERENCE: 4001.002586
CURRENT APPLICATION NUMBER: US/09/561,526
CURRENT APPLICATION NUMBER: 60/131,432
FRIOR PRILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 573
                                                                                     GICCICIAGGCIGCAGGAICICIATAGCAICGIGCGCCGI 210
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Sequence 12, Application US/09561499

Sequence 12, Application US/09561499

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Breaken

TITLE OF INVENTION: ANTHEODY METHODS FOR SELECTIVELY INHIBITING VEGF

FILE REFERENCE: 4001.002582

CURRENT PAPLICANTION NUMBER: US/09/561,499

CURRENT PAPLICATION NUMBER: 60/131,432

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOFFWARE: Patentin Ver: 2.0

SEQ ID NO 12

LENGTH: 573

TYPE: DNA

CORGANISM: Artificial Sequence
                                                44 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArg
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CTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
NOTHER INFORMATION: OLIGONUCLEOTIDE
NAME/EXY: CDS
LOCATION: (1)..(573)
US-09-561-526-12
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Matches:
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        US-09-938-391-4 (1-184) x US-09-561-108-12 (1-573)
                                                                                     151 GGCACCTTCCGGGCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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| Sequence 12, Application US/09561108
| Patent No. 634221
| GENERAL INFORMATION:
| APPLICANT: Philip E. Thorpe
| TILL FOLIONER FOLE A Brekken
| TILL OF INVERTION: ANTHRODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
| FILE REPERENCE: 4001.002584
| CURRENT APPLICATION NUMBER: US/09/561,108
| CURRENT PILING DATE: 2000-04-28
| PRIOR APPLICATION NUMBER: 60/131,432
| PRIOR FILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GGCACCTTCCGGGCTTTCCTGTCCTCTAGGCTGCAGGATCTCTATAGCATCGTGCGCCGT 210
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTHEODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002500
CURRENT APPLICATION NUMBER: US/09/561,500
CURRENT FILING DATE: 2000-04-28
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
ENGIR NO 12
LENGTH: 573
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                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: OLIGONUCLEOTIDE
NAME/KEX: CDS
I. LOCATION: (1)..(573)
US-09-561-500-12
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Matches:
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                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Séquence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 573
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LOCATION: (1)..(573)
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Best Local Similarity:
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Best Local Similarity:
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US-09-561-108-12
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APPLICANT:
APPLICANT:
   Query Match:
DB:
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                                                                                                                                                                                                                                                                                                            44 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArg 63
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08159784
Patent No. 5643783
GENERAL INFORMATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STRRET: 225 Franklin Street
CITY: Boston
                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
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Matches:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 553X
COMPUTER: STREM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
                                                                                                                                                                                                                                       Gaps:
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TELECOMMUNICATION INFORMATION
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23.00
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(617) 542-8906
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: John F. Freeman REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                      ) NAME/KEY: CDS
; LOCATION: (1)..(573)
US-09-561-499-12
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TELEX: 2
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3442 GGCACCTTCCGGGCTTTCCTGTCTCTAGGCTGCAGGATCTCTATAGCATCGTGCGCCGT 3501
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-938-391-4 (1-184) x US-09-620-312D-1012 (1-1823)
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Matches:
Conservative:
Mismatches:
                                                                                                 44 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAsp
                                                           US-09-938-391-4 (1-184) x US-08-159-784-1 (1-4031)
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 AlaGlyLeuAlaGlyThrPheArgAla 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 1012
SEQ ID NO 1012
                                                                                                                                                                                                                                                                                  US-09-620-312D-1012/c
; Sequence 1012, Application US/09620312D
; Patent No. 6569662
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; Sequence 69, Application US/08318193
; Patent No. 5641663
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Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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12.50%
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PLICANT: Liu, Chenghua
PLICANT: Asundi, Vinod
PLICANT: Zhang, Jie
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hao, Qing A.
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Kue, Aidong
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US-09-620-312D-1012
                                                                                                                                                                                 64 AlaAspArg 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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Search completed: August 18, 2003, 03:44:02 Job time : 61.3333 secs
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                                                                                                                                                                                                                                                                                    Score:
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                           AN EXPRESSION SYSTEM FOR THE SECRETION OF BIOACHIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy, Christopher
Guzman, Luz-Maria
VENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
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Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-938-391-4 (1-184) x US-08-318-193-69 (1-508)
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Matches:
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                                                                                                                                                                                                                                     COUNTR: USA
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-222-938A-68
Sequence 68, Application US/09222938A
Patent No. 6437108
Robert T.
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4.35%
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 508 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 508 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                               TITLE OF INVENTION: AN ETITLE OF INVENTION: OF ETITLE OF INVENTION: STIN TITLE OF INVENTION: PROJUMBER OF SEQUENCES: 91 CORRESPONDENCE ADDRESS:
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APPLICANT: Murphy,
APPLICANT: Guzman,
TITLE OF INVENTION:
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Query Match:
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APPLICANT: Youngma
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LOCATION:
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Pred. No.:
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                                                                                                                                                                                                                           COUNTRY:
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Matches:
Conservative:
Mismatches:
Indels:
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        CURRENT APPLICATION NUMBER: US/09/222,938A CURRENT FILING DATE: 1998-12-30 NUMBER OF SEQ ID NOS: 102 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 68 LENGTH: 800
                                                                                                                                                                                                                                                                                                                                                                                                                  156 ArgLeuLeuGluGlnGluAlaAla 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                  760 AGGCTATTAGAGCAAGAAGCAGCA 783
                                                                                                                     TYPE: DNA ORGANISM: Streptococcus pneumoniae
07334/060001
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100.00%
4.35%
                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                      ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (114)...
US-09-222-938A-68
FILE REFERENCE:
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Pred. No.:
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Sequence 37, Appl.
Sequence 12, Appl.
Sequence 45, Appl.
Sequence 46, Appl.
Sequence 1012, Appl.
Sequence 1012, Appl.
Sequence 229171,
Sequence 229171,
Sequence 2294, Appl.
Sequence 2160, Appl.
Sequence 69, Appl.
Sequence 2180, Appl.
Sequence 5313, Appl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/10292418
Sequence 34, Application No. US20030139565A1
FUBLICATION NO. US20030139565A1
GENERAL INFORMATION:
APPLICANT: Li, Yue
APPLICANT: Cillies, Stephen D
TITLE OF INVENTION: Immunofusins
FILE REFERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 1999-08-25
FRIOR APPLICATION NUMBER: 09/383,315
FRIOR FILING DATE: 1999-08-25
FRIOR FILING DATE: 1999-08-25
FRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATCHIN VOY: 2.0
SEQ ID NO 34
LENGTH: 552
                        Sequence 6, Appli
Sequence 59, Appli
Sequence 3, Appli
Sequence 53, Appli
Sequence 30, Appli
Sequence 64, Appli
Sequence 64, Appli
Sequence 1178, Ap
Sequence 144, Appl
Sequence 144, Appl
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Sequence 1, Appli
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Sequence 3, Appli
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Sequence 3, Appli
44444466 40044446
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ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: CDS
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13046
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33719
 US-10-292-418-34
  Command line parameters:

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-DeV=xlp
-D=Cogn2_1/USPTO_spool_p/USPOS938391/runat_04082003_130741_27700/app_query.fasta_1.718
-D=Published_Applications_NA -OFMT=fastap -SUFFIX=p2nol1.rnpb -MINMATCH=0.1
-DOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODELCOAL -OUTFM=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USFR=US09938391 @CCN 1 1 129 @runat 04082003 130741_27700
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPOF=6 -FGAPOF=6 -DELOPE=6 -DELOPE=7
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                                                                                       August 18, 2003, 02:40:12 ; Search time 725.333 Seconds (without alignments) 567.713 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications NA:*

1. /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2. /cgn2_6/ptodata/1/pubpna/PCT_MBW PUB.seq:*
3. /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
4. /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5. /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6. /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
7. /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
8. /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9. /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
11. /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12. /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
11. /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
12. /cgn2_6/ptodata/1/pubpna/USO9_NUBCOMB.seq:*
12. /cgn2_6/ptodata/1/pubpna/USO9_NUBCOMB.seq:*
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                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                  OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                              Title:
Perfect score:
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US-10-131-411-51

Sequence 51, Application US/10131241

Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.

APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer;

TITLE OF INVENTION: Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer;

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer;

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer;

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer;

FILE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer;

FILE OF INVENTION: Compositions and Methods for Info Part: 1999-10-06

FRIOR PELING DATE: 1999-10-06

FRIOR FILING DATE: 1999-05-21

FRIOR PELING DATE: 1999-05-21

FRIOR PELING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Version 3.1

LENGTH: 632

TYPE: DNA

CREANISM: Murinae SP.
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176
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Matches:
Conservative:
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                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  ; ORGANISM: Canine US-10-131-241-50
                                            Alignment Scores: Pred. No.:
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APPLICANT: Holaday, John W.
APPLICANT: Holaday, John W.
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-22
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                 89 GlySerGluGlyGlnLeuLysProGlyAlaArgIlePheSerPheAspGlyArgAspVal 108.
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176
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                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                       1.01e-167
176.00
100.00%
100.00%
95.65%
; LOCATION: (1)..(552)
; OTHER INFORMATION: Endostatin
US-10-292-418-34
                                                                                    Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-131-241-50
                                                           Alignment Scores:
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LENGTH: 552
TYPE: DNA
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Sequence 3, Application US/10292418
| Publication No. US2030139365A1
| GENERAL INFORMATION: US2030139365A1
| APPLICANT: Lo. Kin-Ming
| APPLICANT: Lo. Kin-Ming
| APPLICANT: Li. Yue
| APPLICANT: Gillies, Stephen D
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
| TITLE OF INVENTION: UNMERS: US/10/292,418
| CURRENT FILING DATE: 1999-08-25
| PRIOR APPLICATION NUMBER: US 60/097,883
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Matches:
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                                                PRIOR APPLICATION NUMBER: US 09/315,689
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: US 60/106,343
PRIOR PILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-09-16
PRIOR PILING DATE: 1996-10-22
PRIOR PILING DATE: 1996-10-23
PRIOR PILING DATE: 1996-10-23
PRIOR FILING DATE: 1996-10-23
PRIOR PILING DATE: 1996-10-23
PRIOR PILING DATE: 1996-09-17
CURRENT APPLICATION NUMBER: US/10/042,347 CURRENT FILING DATE: 2002-01-11
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-042-347-4
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Pred. No.:
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US-10-292-418-3
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Sequence 53, Application US/10131241

Bublication No. US20030012792A1

GREEAL INFORMATION:
GREEAL INFORMATION:
APPLICANT: Holaday, John W.
APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer:
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
                                                                                                                                                             121 GGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 180
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Matches:
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Mismatches:
Indels:
                 Conservative:
Mismatches:
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Publication No. US20020183253A1
GENERAL INFORMATION:
APPLICANT: Campochiaro, Peter A.
APPLICANT: Brazzell, Romlus K.
TITLE OF INVENTION: METHOD FOR TREATING OCUL
TITLE OF INVENTION: NEOVASCULARIZATION
FILE REPREMENCE: 4-31881A
CURRENT PILING DÄTE: 2002-02-21
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US-10-080-797-2
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455 GGCTGGCGGCCCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 514
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Sequence 2178, Application US/09880107

Sequence 10. US2002014291A1

SENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

ITILE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR PILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2178
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L22548
US-09-880-107-2178
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Persing, William T.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF PANCREATIC CANCER
TITLE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-391-4 (1-184) x US-09-880-107-2178 (1-3394)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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Query Match:
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Best Local Similarity:
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Pred. No.:
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Fatent No. US20020077289A1

GENERAL INFORMATION:

APPLICANT: MacDonald, Nicholas J.

APPLICANT: Sim, Kim L.

TILE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use

FILE REFERENCE: 05213-0378 (43170-259333)

CURRENT FILING DATE: 2001-06-04

FRIOR APPLICATION NUMBER: US 60/209,065

PRIOR APPLICATION NUMBER: US 60/209,387

PRIOR PILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 123

SEQ ID NO 30

LENGTH: 552
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  ; NUMBER OF SEQ ID NOS: 21
; SOFWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Human
US-10-080-797-2
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Publication No. US20030073144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 GTGCGCCGTGCCGACCGC 197
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Length:
Matches:
Conservative:
Mismatches:
Indels:

574 0 0 0 0

Mismatches: Indels:

Length: Matches: Conservative:

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| GENERAL INVENTION:
| APPLICANT: Lo, Kin-Ming |
| APPLICANT: Li, Yue |
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as |
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as |
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as |
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as |
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as |
| TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as |
| PRIOR PALICATION NUMBER: US 40/93,315 |
| PRIOR PALLING DATE: 1999-08-25 |
| PRIOR PAPLICATION NUMBER: US 60/097,883 |
| PRIOR PAPLING DATE: 1999-08-25 |
| NUMBER OF SEQ ID NOS: 54 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO 17 |
| LENGTH: 552 |
| TYPE: DNA |
| TYPE: DNA |
| ORGANISM: Mus musculus |
| CREANISM: Mus musculus |
| CREANISM: Mus musculus |
| CREANISM: Muscu
                                                                                                                                                                                                                                                                                                                                                                     44 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArg
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Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 17, Application US/10292418; Publication No. US20030139365A1
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NAME/KEY: CDS
LOCATION: (1)..(552)
COTHER INFORMATION: endostatin
US-10-292-418-17
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  ORGANISM: Rhesus monkey
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                      US-10-131-241-48
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APPLICANT: Fortier, Anne H.
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
TILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4120 GGGCTGGCGGGCACCTTCCGCGCCTTCCTGTCCTCGCGCCTGCAGGACCTGTACAGCATC 4179
41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 60
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodges, Michael J.
APPLICANT: Lodges, Michael J.
APPLICANT: Dereing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yugiu
TITLE OF INVENTION: COMFOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENY APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                    ; Sequence 144, Application US/10060036; Publication No. US20030073144A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 48, Application US/10131241; Publication No. US20030012792A1; GENERAL INFORMATION:
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                                                                                                            61 ValArgArgAlaAspArg 66
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US-10-131-241-48
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LENGTH: 540
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CB443805 694911 MA
BG823096 602726433
BM488074 pgm2n.pk0
BU495935 603367327
BU35206 603527927
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BU290652 604164521
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BU268246 603507092
BU268246 603507164
BU380308 603502164
BU380308 603502164
BU380308 11 H-E21-
BU77348 U1 H-BT1-
BU5520 x H2610.x
BU632049 U1 H-FE1-
BU63520 U1 H-FE1-
BU63520 U1 H-FE1-
BU63520 U1 H-FE1-
BU63520 U1 H-FE1-
BU615520 U1 H-FE1-
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BUS56872 AGENCOURT
BQ673186 AGENCOURT
CB537919 775852 MA
BF117397 uz36e11.y
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BB906253 GO1502237
BG387051 602463749
BU540812 AGENCOURT
CD105862 AGENCOURT
B1161007 602865213
BQ672290 AGENCOURT
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BG383970 302444 MA
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Mammalia; Eutheria, Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 451)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
                                                                                                                                  AW464343 BP230015B
                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                           SUMMARIES
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AW192502
BU632049
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BU485669
AV660284
CB216999
BU158380
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CD105862
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BG383970
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BU230900
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CB444165
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BF601253
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BM488074
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Sus scrofa
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Query
Match 1
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BG383960
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
                                                                                Result
No.
                                                                                                                                                                                                                               August 18, 2003, 00:28:06; Search time 1631.11 Seconds (without alignments) 2741.704 Million cell updates/sec
                                                                                                                          184
1 HTHQDFQLVLHLVALNSPQP......CRHAFVVLCIENSVMTSFSK 184
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          GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                   - nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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60.0 , Ygapext 60.0
6.0 , Fgapext 7.0
6.0 , Delext 7.0
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Maximum DB seq length: 200000000
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Perfect score:
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                                                   OM protein
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                                                                                                                                                                                                                                         Word size:
                                                                                                                                     Sequence:
                                                                                                                                                                                                                      Searched:
                                                                       Run on:
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
DO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing: Bases called and alt_trimmed with phred
and —minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW464343 24-FBB-2000 BP230015B10C11 Soares normalized bovine placenta Bos taurus cDNA clone BP230015B10C11 5', mRNA sequence.
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1 (bases 1 to 279)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 GGCCAGCTGAAGCCCGGCGCCCGCATCTTCTCTTTCGACGCAGAGACGTCCTTCAGCAC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled"
/lab.host="DH10B"
/clone lib="WARC IPIG"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site_2: Sal1;
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/note="Vector: pCMV SPORT6; Site_2: Sal1; Sal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 ValAsnLeuArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGlu
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Conservative:
Mismatches:
Indels:
  EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
22213789
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/mol_type="mRNA"
/db_xref="taxon:9823"
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Plate: 89 row: K column: 13
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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Unpublished
Contact: Lewin, H. A.
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                                                                                                                                                                                                                                                                                                                                                             PCR PRimers
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Query Match:
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Pred. No.:
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/ Organism="Gus scrofa"

/ Mol_Lype="mRNA"

/ Mb_xref="taxon:9823"

/ Lissue Lype="pooled"

/ Lab_hogt="DH108"

/ Clone lib="MARC IPIG"

/ note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;

Library made from pooled tissue from day 11, 13, 15, 20,

and 30 embryos. 15. 271 t
                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tal: 402 762 4396
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R., Quackenbush,J. and Keele,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly 475-478 (2002)
22213789
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Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Quackenbush, J. and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValAsnLeuArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGlySerGlu
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Matches:
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Mismatches:
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 89 row. I column: 13
Seq primer: ATPRAGGTGACACTATAG
Location/Qualifiers
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Sus scrofa (pig)
Sus scrofa
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Best Local Similarity:
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BG383970
LOCUS
DEFINITION
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AUTHORS
                                                                                                            JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
1 (bases 1 to 623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GECACCTTCCGCGCGTTCCTCTCCCGCGTTGCAGGACCTGTACAGCATCGTGCGCCCC 165
                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called and alt_trimmed with phred v0.880904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.

PCR PRIMERS
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.C Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from testis, thymus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 ArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAlaGlyLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIleValArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        semitendonosus muscle, longissimus muscle, pancreas,
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43
0
0
0
                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .551
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-938-391-4 (1-184) x BF074459 (1-551)
                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 81 row: F column: 9
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43.00
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Best Local Similarity:
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CB424313/c
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KEYWORDS
SOURCE
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                                                                                        Tel: 217 244 5617
Email: h-lewin@uluc.edu
Funding for cattle EST sequencing was provided by the USDA National
Fesearch Initiative, Animal Genome Resource Grant AG 99-3205-8834
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone..../
/lab_nost="DH10B"
/lab_nost="DH10B"
/clone_lib="Soares normalized bovine placenta"
/clone_lib="Soares normalized bovine placenta"
/clone_lib="Soares normalized bovine placenta"
/clone_lib="Soares normalized by the Ste_2: Not!; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "
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1 (bases 1 to 551)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 SerGluGlyGlnLeuLysProGlyAlaArgllePheSerPheAspGlyArgAspValLeu 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 TCCGAGGGCCAGCTGAAGCCCGGCGCCCGCATCTTCTCCTTCGACGCAGAGATGTCCTT 257
                                                   I
       W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 ProValValAsnLeuArgAspGluValLeuPheProSerTrpGluAlaLeuPheSerGly
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0 0 0 0 0 0 0
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                            column: 11
                                                                                                                                                                                                                                                                                                                      FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCTCACATAAAG
INSERT LENGTH: 279 Std Error: 0.00
Plate: BP230015B10 row: C column: 1
Seq primer: ACCGACATAACAATTCACACAGA
High quality sequence stop: 279.
Location/Qualifiers
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Matches:
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/db_xref="taxon:9913"
/clone="BP230015B10C11"
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BF074459.1 GI:10867970
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Bos taurus
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Best Local Similarity:
                                                                        61801, USA
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Pred. No.:
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Query Match: DB:

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No.:

Score:

BASE COUNT

ORIGIN

source

FEATURES

DEFINITION ACCESSION VERSION

RESULT 4 BF074459

LOCUS

ORGANISM

KEYWORDS SOURCE

AUTHORS

REFERENCE

105

63

TITLE

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Single page sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: FQY8051 row. I column: 11
Seq primer: GTAATACGACTATAGGG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 709)
Smith,T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 25-MAR-2003
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                      /tissue_type="pooled"
/lab_host="PH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made_with RNA pooled_from multiple_tissues
-including_liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
a 217 c 219 g 113 t 1 others
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694911 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
CB443805
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4390
Fax: 402 762 4390
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                       /organism="Bos taurus"
                                                                                                      Seq primer: TAGAAGGCACAGTCGAGG.
Location/Qualifiers
                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                              107
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CB443805
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                                                                                                                                                                                   Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: FQX8006 row: I column: 12
Seq primer: TAGAAGGCACAGTCGAGG.
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1 (bases 1 to 657)
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W.
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
way,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished
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                                                                                                                                                                                                                                                                                                                                      /moi_type="mona"
//db zref="taxon:9913"
/db zref="taxon:9913"
/lab_host="type="pooled"
/lab_host="bH108"
/clone lib="Marc GBOW"
/note="vector: pcDNA3.1; Site 1: EcoR1; Site 2: Not1; Library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium:
placenta/endometrium:
placenta/endometrium:
placenta/endometrium:
placenta/endometrium:
placenta/endometrium:
placenta/endometrium:
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CB444165
CB444165.1 GI:29233914
EST.
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443
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                                                                                        USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4369 Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PD DA 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
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                                                                          Contact: Smith TPL
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Bos taurus
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Best Local Similarity:
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Matches:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4865936"
                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                         /mol type="mRNA"
/db xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
                 1. .387
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                  US-09-938-391-4 (1-184) x BF601253 (1-387)
Location/Qualifiers
                                                                                                                                                                                               131 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence. _ _ BG823096
BG823096.1 GI:14170683
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TITLE
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.

Bovidae; Bovinae; Bos.

1 (bases 1 to Sosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 25-APR-2001
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                                                            /tissue_type="pooled"
/lab_host="pooled"
/lab_host="Pullug"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoR1; Site_2: Not1;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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43
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                 Indels:
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                 organism="Bos taurus"
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BACKWARD: GTTTCCCAGTCACGACG
Plate: 40 row: H column: 7
Seq primer: ATTTAGGTGACACTATAG.
                               /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                 US-09-938-391-4 (1-184) x CB443805 (1-709)
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PCR PRimers
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Fax: 402 762 4390
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PUBMED
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BF601253
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BG823096 483 bp mRNA linear EST 22-MAY-2001
602726433F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4865936 5',
/clone_lib="WARC 3BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
/instary made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 15"
/note="Yogan: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
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I (basea I to 483)

NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLCM1732 row: a column: 09
High quality sequence stop: 479.
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BM488074 GI:18609005
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Alab host="E. coli EMCHIOB"
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/note="Vector: pCMVSPORT6; Library made from equivalent
                                                                                                                                                                                                                                                                                                                                                   270 GGCGGCATGCGGGGGCCGACTTCCAGTGCTTCAGCAGCGCGCGGGGCCGCT 329
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"
                                                                                                                                                                                                                                                                                      GlyGlyMetArgGlyIleArgGlyAlaAspPheGlnCysPheGlnGlnAlaArgAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 577)
Cogburni.L.A. and Monsonego-Ornan,E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
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/mol_type="mRNA"
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/sex="Male and Female"
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/dev stage="adult"
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/clone_lib="CSEQRBNI"
/clone_lib="CSEQRBNI"
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ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters; digested with ECORI
, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
Phasianinae; Gallus.
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BU459935 614 bp mRNA linear EST 29-NOV-2002 603367327F1 CSEQRBN19 Gallus gallus cDNA clone ChEST268f8 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
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/mol_type="mRNA"
/strain="Layer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Simon. Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manchester, M60 1QD,
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/clone="ChEST268f8"
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               rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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1 (bases I to 653)

Boardman, P.E., Sana-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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University of Manchester Institute of Science and Technology (UMIST
pBluescript (KS+) vector. The library was normalized in 2
                                                                                                                                                                                                                                                                                                                                                                                                                 183 GGGCTGGCCGGTACCTTCCGTGCCTTCCTCCTCCCCGCCTGCAGGACCTGTACAGCATC 242
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/mol_type="mRNA"
/strain="Compton Line 151"
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/lab_host="DH10B"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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Gallus gallus
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VERSION

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, size-selected, and cloned into the NotI and ECORI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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/clone_lib="Normalized chicken muscle cDNA library (pgm2n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler chickens, Ottawa Research Ctr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 GGGCTGGCCGGTACCTTCCGTGCCTTCCTCCTCCCCGCCTGCAGACCTGTACAGCATC 280
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
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Cogburn, L.A. and Monsonego-Ornan, E.
Chicken ESTs from muscle
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/clone="pgm2n.pk013.n20"
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KS(+); Site_l: EcoRI; Site_2: Not1; This normalized
library was Constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NoI adapters, digested with EcoRI
compabible sites of a custom modified MCS of the
pBluescript (KS4) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
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Gallus gallus 3

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Mesazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Phasianinae; Gallus.

1 (Basea I to 686)

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W. T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehenaive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                     bp mRNA linear EST 27-NOV-2002
gallus cDNA clone ChEST1021j6 5', mRNA
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University of Manchester Institute of Science and Technology (UMIST
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Fax: 01612360409
Email: Simon-Hubbard@umist.ac.uk.
Location/Qualifiers
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//clone lib="Vector: pBluescript II KS(+); Site_1: ECCRI;
Site_2: Nort; This normalized library was—constructed from site_2: nort; primer clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EccRI, size-selected, and cloned into the NotI and ECCRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BU439577 706 bp mRNA linear EST 29-NOV-2002 603208252F1 CSEQRBN11 Gallus gallus cDNA clone ChEST183g14 5', mRNA
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1 (bases 1 to 706)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. Curr. Biol. 12 (22), 1965-1969 (2002)
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(1996): 791, except that a significantly longer reannealing hybridization was used."
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strain="Layer and broiler"
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/clone="ChEST183914"
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Location/Qualifiers
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Gallus gallus
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adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

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41 GlyLeuAlaGlyThrPheArgAlaPheLeuSerSerArgLeuGlnAspLeuTyrSerIle 60

US-09-938-391-4 (1-184) x BU439577 (1-706)

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